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(71) Applicants *(for all designated States except US)*: **CURAGEN CORPORATION** [US/US]; 11th Floor, 555 Long Wharf Drive, New Haven, CT 06511 (US). **BIOGEN, INC.** [US/US]; 14 Cambridge Center, Cambridge, MA 02142 (US).

[Continued on next page]

(54) Title: NOVEL POLYNUCLEOTIDES EXPRESSED IN ACTIVATED T-LYMPHOCYTES AND PROTEINS ENCODED THEREBY

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Translated Prctein - Frame: 1 - Nucleotide 1 to 2586

  1 ATGATGAAGACGGAGCCACGGGGGCCCGGGGGTCCCCTCCGGAGC
    MetMetLysThrGluProArgGlyProGlyGlyProLeuArgSer

 46 GCCTCCCCGCACCGCAGCGCCTACGAGGCGGGCATCCAGGCGCTG
    AlaSerProHisArgSerAlaTyrGluAlaGlyIleGlnAlaLeu

 91 AAGCCGCCCGACGCGCCCGGGCCCGACGAGGCACCCAAGGGGGCC
    LysProProAspAlaProGlyProAspGluAlaProLysGlyAla

136 CACCACAAGAAATATGGCTCCAACGTCCACCGCATCAAAAGTATG
    HisHisLysLysTyrGlySerAsnValHisArgIleLysSerMet

181 TTCCTGCAGATGGGCACGACGGCGGGGCCCTCGGGCGAGGCGGGC
    PheLeuGlnMetGlyThrThrAlaGlyProSerGlyGluAlaGly

226 GGCGGCGCGGCCCTGGCCGAGGCCCCACGGGCGTCCGAGCGCGGC
    GlyGlyAlaGlyLeuAlaGluAlaProArgAlaSerGluArgGly

271 GTGCGCCTGTCGCTGCCGCGGGCCAGCAGCCTGAACGAGAACGTG
    ValArgLeuSerLeuProArgAlaSerSerLeuAsnGluAsnVal

316 GACCACAGCGCCCTGCTGAAGCTGGGCACCAGCGTGTCGGAGCGC
    AspHisSerAlaLeuLeuLysLeuGlyThrSerValSerGluArg

361 GACCGGAAGCTGGACGTCGTGGTGCGCTTCAACGGCAGCACCGAG
    AspArgLysLeuAspValValValArgPheAsnGlySerThrGlu

406 GCGCTGGACAAGCTGGACGCTGACGCCGTGTCCCCCACGGTCAGC
    AlaLeuAspLysLeuAspAlaAspAlaValSerProThrValSer

451 CAGCTCAGCGCCGTCTTCGAGAAGGCCGACTCGAGGACCGGCCTC
    GlnLeuSerAlaValPheGluLysAlaAspSerArgThrGlyLeu

496 CACCGCGGGCCCGGGCTCCCCAGGGCCGCAGGGGTTCCCCAGGTC
    HisArgGlyProGlyLeuProArgAlaAlaGlyValProGlnVal

541 AACTCGAAGCTGGTCAGCAAGCGGTCCCGGGTGTTCCAGCCCCCG
    AsnSerLysLeuValSerLysArgSerArgValPheGlnProPro

586 CCGCCGCCGCCGCCCGCCCCGTCGGGGGATGCCCCGGCCGAGAAA
    ProProProProProAlaProSerGlyAspAlaProAlaGluLys

631 GAGCGATGCCCCGCAGGGCAGCAGCCCCCGCAGCACCGAGTGGCC
    GluArgCysProAlaGlyGlnGlnProProGlnHisArgValAla

676 CCTGCCCGGCCGCCCCCCAAGCCCCGGGAGGTGCGCAAGATTAAG
    ProAlaArgProProProLysProArgGluValArgLysIleLys
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(57) Abstract: Disclosed are four novel human nucleic acid sequences expressed in activated T-lymphocytes. Also provided are polypeptides encoded by these nucleic acid sequences, and antibodies that immunospecifically bind to a polypeptide of the invention, or any derivative, variant, mutant or fragment of the polypeptide, polynucleotide or antibody. The invention further provides therapeutic, diagnostic and research methods for treating and diagnosing disorders related to these novel human T-lymphocyte proteins.

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(72) **Inventors; and**
(75) **Inventors/Applicants** *(for US only)*: **PEYMAN, John, A.** [US/US]; 336 West Rock Avenue, New Haven, CT 06515 (US). **GREEN, Cynthia, D.** [US/US]; 29 Twin Bridge Road, Madison, CT 06443 (US). **HSU, Andro** [US/US]; 412 Orange Street, New Haven, CT 06511 (US). **BROWNING, Jeffrey, A.** [US/US]; 32 Milton Road, Brookline, MA 02446 (US). **CARULLI, John** [US/US]; 9 Harris Drive, Southborough, MA 01772 (US).

(74) **Agent: ELRIFI, Ivor, R.**; Mintz, Levin, Cohn, Ferris, Glovsky, and Popeo, P.C., One Financial Center, Boston, MA 02111 (US).

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NOVEL POLYNUCLEOTIDES EXPRESSED IN ACTIVATED T-LYMPHOCYTES AND PROTEINS ENCODED THEREBY

FIELD OF THE INVENTION

The invention relates in general to nucleic acids and polypeptides and more particularly to polynucleotides expressed in activated T-lymphocytes, and polypeptides encoded by such polynucleotides, as well as vectors, host cells, antibodies and recombinant methods for producing the polypeptides and polynucleotides.

BACKGROUND OF THE INVENTION

The mammalian immune system can be characterized by cell-mediated immune responses and antibody mediated immune responses. Cell-mediated immune responses are effected by a type of lymphocyte known as a T lymphocyte.

For a T lymphocyte to mount a productive response to an antigen, it must recognize an antigen that is presented by an MHC class I or class II-expressing cell. T cells typically do not respond to an antigen until they are activated. A failure of a T cell to be properly activated, or, conversely, inappropriate activation of a T cell, can result in deleterious consequences to an individual.

Not all the genes associated with T cell activation have been identified.

SUMMARY OF THE INVENTION

The present invention is based, in part, on the discovery of novel polynucleotide sequences expressed in activated T lymphocytes. These activated T lymphocyte associated sequences (herein "ATLAS") include ATLAS-1, a novel phosphatase regulator, ATLAS-2, A novel cytokine receptor, ATLAS-3, a novel member of the thioredoxin and protein disulfide isomerase family, and ATLAS-4, a novel protein with homology to a putative multiple sclerosis aetiologic agent. Collectively the ATLAS-1, ATLAS-2, ATLAS-3, and ATLAS-4 nucleotide sequences are referred to herein as "ATLAS-X".

In one aspect, the invention provides an isolated nucleic acid molecule encoding a polypeptide that includes an amino acid sequence of a polypeptide that is at least 90% identical

to an ATLAS-X polypeptide. In some embodiments, the nucleic acid molecule can hybridize under stringent conditions to a nucleic acid sequence complementary to a nucleic acid molecule that includes a protein-coding sequence of an ALTAS-X nucleic acid sequence.

Also included in the invention is an oligonucleotide, *e.g.*, an oligonucleotide less than 100 nucleotides in length that includes at least 6 contiguous nucleotides of an ATLAS-X nucleic acid, *e.g.*, SEQ ID NO:1, or a complement of the oligonucleotide.

Also included in the invention is substantially purified ATLAS-X polypeptide. In some embodiments, the ATLAS-X polypeptide includes an amino acid sequence at least 80% identical to a polypeptide that includes the amino acid sequence of SEQ ID NO:2, 4, 6, or 8.

The invention also features an antibody that selectively binds to an ATLAS-X polypeptide.

In another aspect, the invention includes a pharmaceutical composition which includes a therapeutically or prophylactically effective amount of a therapeutic and a pharmaceutically acceptable carrier. The therapeutic can be, *e.g.*, an ATLAS-X nucleic acid, and ATLAS-X polypeptide, or an antibody to an ATLAS-X polypeptide. In a further aspect, the invention includes, in one or more containers, a therapeutically or prophylactically effective amount of this pharmaceutical composition.

In a further aspect, the invention includes a method of producing a polypeptide by culturing a cell that includes an ATLAS-X nucleic acid, *e.g.*, an ATLAS-X DNA, under conditions allowing for expression of the ATLAS-X polypeptide encoded by the DNA. If desired, the ATLAS-X polypeptide can then be recovered.

In another aspect, the invention includes a method of detecting the presence of an ATLAS-X polypeptide in a sample. In the method, a sample is contacted with a compound that selectively binds to the polypeptide under conditions allowing for formation of a complex between the polypeptide and the compound. The complex is detected, if present, thereby identifying the polypeptide in the sample.

Also included in the invention is a method of detecting the presence of an ATLAS-X nucleic acid molecule in a sample by contacting the sample with an ATLAS-X nucleic acid probe or primer, and detecting whether the nucleic acid probe or primer bound to an ATLAS-X nucleic acid molecule in the sample.

In a further aspect, the invention provides a method for modulating the activity of an ATLAS-X polypeptide by contacting a cell sample that includes an ATLAS-X polypeptide with a compound that binds to the polypeptide in an amount sufficient to modulate the activity of the polypeptide. The compound can be, *e.g.*, a small molecule, such as a nucleic acid, peptide, polypeptide, peptidomimetic, carbohydrate, lipid or other organic (carbon containing) or inorganic molecule, as further described herein.

Also within the invention is the use of a therapeutic in the manufacture of a medicament for treating or preventing a syndrome associated with a human immune system disorder. The therapeutic can be, *e.g.*, an ATLAS-X nucleic acid, and ATLAS-X polypeptide, or an ATLAS-X antibody.

The invention further includes a method for screening for a modulator of an immune disorder. The method includes contacting a test compound with an ATLAS-X polypeptide and determining if the test compound binds to the polypeptide. Binding of the test compound to the polypeptide indicates the test compound is a modulator of activity, or of latency or predisposition to an immune disorder.

Also within the invention is a method for screening for a modulator of activity, or of latency or predisposition to an immune disorder by administering a test compound to a test animal at increased risk for the disorder. The test animal expresses a recombinant polypeptide encoded by an ATLAS-X nucleic acid. Expression or activity of the ATLAS-X polypeptide is then measured in the test animal, as is expression or activity of the protein in a control animal that recombinantly expresses the protein and is not at increased risk for the disorder. Next, the expression of the protein in the test animal and the control animal is compared. A change in the activity of the protein in the test animal relative to the control animal indicates the test compound is a modulator of latency of the disorder. Preferably, the disorder is an autoimmune disorder, an immune disorder, a T-lymphocyte-associated disorder, a cell-proliferation disorder, a cell differentiation disorder, or an immune deficiency order.

In another aspect, the invention includes a method for determining the presence of or predisposition to a disease associated with altered levels of an ATLAS-X polypeptide, an ATLAS-X nucleic acid, or both, in a subject, *e.g.*, a human subject. The method includes measuring the amount of the polypeptide in a test sample from the subject and comparing the amount of the polypeptide in the test sample to the amount of the polypeptide present in a

control sample. An alteration in the level of the polypeptide in the test sample as compared to the control sample indicates the presence of or predisposition to a disease in the subject.

In a further aspect, the invention includes a method of treating or preventing a pathological condition associated with an immune system disorder in a mammal by administering to the subject an ATLAS-X polypeptide, an ATLAS-X nucleic acid, or an ATLAS-X antibody to a subject, *e.g.*, a human subject, in an amount sufficient to alleviate or prevent the pathological condition. In some embodiments, the immune system associated disorder is an autoimmune disorder, an immune disorder, a T-lymphocyte-associated disorder, a cell-proliferation disorder, a cell differentiation disorder, or an immune deficiency disorder.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A-1D are a representation of a nucleic acid sequence (SEQ ID NO:1) and an encoded amino acid sequence (SEQ ID NO:2) of ATLAS-1 nucleic acids and polypeptides according to the invention.

Figures 2A-2H are a representation of a nucleic acid sequence (SEQ ID NO:3) and an encoded amino acid sequence (SEQ ID NO:4) of ATLAS-2 nucleic acids and polypeptides according to the invention.

Figures 3A-3B are a representation of a nucleic acid sequence (SEQ ID NO:5) and an encoded amino acid sequence (SEQ ID NO:6) of ATLAS-3 nucleic acids and polypeptides according to the invention.

Figures 4A-4B are a representation of a nucleic acid sequence (SEQ ID NO:7) and an encoded amino acid sequence (SEQ ID NO:8) of ATLAS-4 nucleic acids and polypeptides according to the invention.

DETAILED DESCRIPTION OF THE INVENTION

The present invention is based, in part, upon the discovery of nucleic acids encoded in activated T lymphocytes and of polypeptides encoded by these nucleic acids. The nucleic acids have been named "Activated T Lymphocyte Associated Sequences 1-4", or collectively, "ATLAS-X". Representative ATLAS-X sequences, and examples of uses of these sequences, are next briefly discussed.

1. ATLAS-1: A novel phosphatase regulator

An ATLAS-1 sequence according to the invention includes a nucleotide sequence encoding a polypeptide related to previously described phosphatase regulators. A representation of an ATLAS-1 nucleic acid sequence according to the invention, and a polypeptide sequence encoded by this nucleic acid sequence, is shown in Figures 1A-1D. The sequence in Figures 1A-1D includes a nucleotide sequence of 3290 nucleotides (SEQ ID NO:1). Nucleotides 1 to 2586 define an open reading frame encoding a polypeptide of 862 amino acid residues (SEQ ID NO:2). An ATLAS-1 nucleotide sequence according to the invention is also present in clone 5.02w0c0-60.3. An ATLAS-1 gene is localized to human chromosome 17.

The calculated molecular weight of the ATLAS-1 protein is 94,019.9 daltons. The protein contains four to six hydrophobic regions. Using BLASTP protein comparison analysis, the predicted protein is 89% homologous (266 aa/296 aa) to rat neurabin II (see, *e.g.*, J. Biol. Chem. 273 (6), 3470-3475 (1998)) and 68% homologous (407 of 594 aa) to rat spinophilin (see, *e.g.*, Proc. Natl. Acad. Sci. U.S.A. 94 (18), 9956-9961 (1997). Rat spinophilin is reported to modulate the activity of protein phosphatase-1 in neurons.

Based on its relatedness to neurabin and spinophilin, at least one use of an ATLAS-1 protein of the invention is as a novel phosphatase regulator expressed in activated T lymphocytes. Thus, the ATLAS-1 protein may modulate, *e.g.*, stimulate or suppress, activation

of T-lymphocytes. The ATLAS-1 polypeptide, or nucleic acids encoding the ATLAS-1 polypeptide, can be used to identify small molecule agonists and antagonists. The natural substrate(s) of this novel phosphatase regulator may likewise be used in methods of modulating, *e.g.*, stimulating or suppressing the activation of T lymphocytes, and may similarly be used to identify compounds, *e.g.*, small molecule agonists and antagonists of immune responses.

2. ATLAS-2: A novel cytokine receptor

An ATLAS-2 nucleic acid sequence according to the invention includes a nucleotide sequence that encodes a polypeptide related to previously described cytokine receptors. Figures 2A-2H include a representation of an ATLAS-2 nucleic acid sequence of the invention, and a polypeptide sequence encoded by this polypeptide. The disclosed nucleic acid sequence is 6461 nucleotides in length (SEQ ID NO:3), of which nucleotides 1 to 5553 define an open reading frame encoding a polypeptide of 1851 amino acids (SEQ ID NO:4). An ATLAS-2 nucleotide sequence according to the invention is also present in clone 5.02r011-102.5. The sequences localize to human chromosome 11p15.5.

The calculated molecular weight of the protein in Figures 2A-2H is 202,523 daltons. The protein includes about 20 hydrophobic regions, which may be transmembrane segments. According to protein analysis results ("BLASTP"), the predicted protein is 52% identical (250 aa/ 458 aa) to rat vasopressin receptor (GenBank Accession Number q63035). It is 37% identical (98 aa/ 263 aa) to human angiotensin/vasopressin receptor (GenBank Accession Number o75434).

Based on its relatedness to rat vasopressin receptor and human angiotensin/vasopressin receptor, the ATLAS-2 protein is likely a novel member of the cytokine receptor family. Blocking antibodies raised to this putative receptor, which is expressed in activated T lymphocytes, are useful for modulating, *i.e.*, stimulating or suppressing, T lymphocyte effector functions. The receptor can also be used to identify ligand(s) which may be immunosuppressive or immunostimulatory. The receptor may be also be used to identify compounds, *e.g.*, small molecule agonists or antagonists, which may be immunosuppressive or immunostimulatory.

3. ATLAS-3: A novel member of the thioredoxin and protein disulfide isomerase family

An ATLAS-3 nucleic acid according to the invention includes nucleotide sequence of 2564 base pairs in length (SEQ ID NO:5) shown in Figures 3A-3B. Also shown in Figures 3A-3B is a polypeptide of 269 amino acid residues (SEQ ID NO:6) that is translated from nucleotides 98 to 904 of SEQ ID NO:5. An ATLAS-3 nucleic acid sequence is also present in clone 5.02r011-149.

The calculated molecular weight of the predicted protein is 30,045 daltons. The protein has an endoplasmic reticulum retention signal and the subcellular localization is probably in the endoplasmic reticulum (ER). According to protein analysis results ("BLASTP"), the predicted protein is 43% identical to mouse and human protein disulfide isomerase (GenBank Accession Numbers p27773 [mouse] and p30101 [human]). Protein disulfide isomerases are endoplasmic reticulum resident proteins with KDEL targeting signals.

Based on its relatedness to protein disulfide isomerases, the disclosed ATLAS-3 protein is a novel member of the thioredoxin or protein disulfide isomerase family.

Two domains in the disclosed ATLAS-3 protein additionally resemble thioredoxin. The thioredoxins act in DNA synthesis as dithiol hydrogen donors. Thioredoxins are involved in the regulation of metabolic processes, such as growth regulation, enzyme modulation, receptor activity, or transcriptional regulation.

An ATLAS-3 protein may act as a protein-folding chaperone to modulate T lymphocyte activation. Alternatively, or in addition, the ATLAS-3 protein may act as a growth regulator similar to thioredoxin. For example, the ATLAS-3 protein may act on T lymphocyte substrates.

The ATLAS-3 protein may also be used to identify compounds, *e.g.*, small molecules, which can regulate (stimulate or suppress) an immune response. In addition, the ATLAS-3 protein can be used to identify secreted substrate protein or proteins in T lymphocytes, which themselves may be immunoregulatory.

4. ATLAS-4: A novel protein with homology to a putative multiple sclerosis aeti logic agent

An ATLAS-4 nucleic acid according to the invention includes a nucleotide sequence of 1828 nucleotides (SEQ ID NO:7), as shown in Figures 4A-4B. Figures 4A-4B also show a polypeptide of 358 amino acid residues (SEQ ID NO:8) that is translated from nucleotides 1 to 1074 of SEQ ID NO:7. An ATLAS-4 nucleic acid sequence according to the invention is also present as clone 5.02h0n0-103.1.

The calculated molecular weight of the protein is 38,133 daltons. A putative signal sequence of 28 hydrophobic residues is present at amino acids 1 to 128 with one hydrophobic residue. The 80 residues are at the amino- and carboxy-terminus of the protein are similar. These domains contain five evenly spaced charged residues as well as two cysteine residues.

BLASTP sequence analysis indicates that the predicted protein is 69% (65 aa/ 94 aa) similar to a portion of sequence for multiple sclerosis associated retrovirus-1 (MSRV-1, described on WO9823755-A1). ClustalW analysis indicates that the ATLAS-4 protein is also similar to portions of seven related peptides encoded by MSRV-1 (which is discussed in WO9823755-A1, FR2762601-A1 and WO9706260).

The disclosed ATLAS-4 nucleic acid sequence localizes to human chromosome 1q23.3-24.3.

Based on its homology to MSRV-1 protein, an ATLAS-4 protein of the invention may act in T lymphocytes to modulate immune function, *e.g.*, in stimulation or suppression of immune responses.

A summary of the ATLAS nucleic acid sequences, encoded polypeptides, as well as sequence identifier numbers (SEQ ID NOs) corresponding to various disclosed sequences and clones containing these nucleic acids is shown in Table 1. As used herein, "ATLAS-X" corresponds to any of ATLAS-1, ATLAS-2, ATLAS-3 or ATLAS-4.

Table 1: Sequences and Corresponding SEQ ID Numbers of Disclosed Sequences

Atlas X	Isolate Number	Sequence Identifier Number	Sequence Identifier Number of Encoded Polypeptide Sequence	Putative Function
ATLAS1	5.02w0c0-60.3	SEQ ID NO:1	SEQ ID NO:2	Phophatase Regulator
ATLAS2	5.02r011-102.5.	SEQ ID NO:3	SEQ ID NO:2	Cytokine Receptor
ATLAS3	5.02r011-149	SEQ ID NO:5	SEQ ID NO:6	Thioredoxin/Protein Disulfide Isomerase
ATLAS4	5.02h0n0-103.1	SEQ ID NO:7	SEQ ID NO:8	Multiple Sclerosis Aetiologic Agent

ATLAS-X Nucleic Acids

One aspect of the invention pertains to isolated nucleic acid molecules that encode ATLAS-X polypeptides or biologically active portions thereof. Also included in the invention are nucleic acid fragments sufficient for use as hybridization probes to identify ATLAS-X-encoding nucleic acids (*e.g.*, ATLAS-X mRNA) and fragments for use as PCR primers for the amplification or mutation of ATLAS-X nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

"Probes" refer to nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or as many as about, *e.g.*, 6,000 nt, depending on use. Probes are used in the detection of identical, similar, or complementary nucleic acid sequences.

Longer length probes are usually obtained from a natural or recombinant source, are highly specific and much slower to hybridize than oligomers. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies.

An "isolated" nucleic acid molecule is one that is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated ATLAS-X nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (*e.g.*, lymphocytes, *e.g.*, activated T lymphocytes). Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 10, 11, 12, or a complement of any of these nucleotide sequences, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequence of SEQ ID NO:1, 3, 5, or 7 as a hybridization probe, ATLAS-X molecules can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook *et al.*, (eds.), MOLECULAR CLONING: A LABORATORY MANUAL 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; and Ausubel, *et al.*, (eds.), CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993.)

A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to ATLAS-X nucleotide sequences can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

As used herein, the term "oligonucleotide" refers to a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or complementary DNA or RNA in a particular cell or tissue. Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at lease 6 contiguous nucleotides of SEQ ID NO:1, 3, 5, 7, or a complement thereof. Oligonucleotides may be chemically synthesized and may be used as probes.

In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in SEQ ID NO:1, 3, 5, or 7, or a portion of this nucleotide sequence, *e.g.*, a fragment that can be used as a probe or primer or a fragment encoding a biologically active portion of ATLAS-X. A nucleic acid molecule that is complementary to the nucleotide sequence shown in SEQ ID NO:1, 3, 5, or 7 is one that is sufficiently complementary to the nucleotide sequence shown in SEQ ID NO:1, 3, 5, or 7 that it can hydrogen bond with little or no mismatches to the nucleotide sequence shown in SEQ ID NO:1, 3, 5, or 7, thereby forming a stable duplex.

As used herein, the term "complementary" refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term "binding" means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, van der Waals, hydrophobic interactions, etc. A physical interaction can be either direct or indirect. Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

Fragments provided herein are defined as sequences of at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively, and are at most some portion less than a full length sequence.

Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice. Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but differs from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type. Homologs are nucleic acid sequences or amino acid sequences of a particular gene that are derived from different species.

Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the invention, in various embodiments, by at least about 30%, 50%, 70%, 80%, or 95% identity (with a preferred identity of 80-95%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions. See *e.g.* Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993, and below.

A "homologous nucleic acid sequence" or "homologous amino acid sequence," or variations thereof, refer to sequences characterized by a homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of ATLAS-X polypeptide. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA. Alternatively, isoforms can be encoded by different genes. In the present invention, homologous nucleotide sequences include nucleotide sequences encoding for an ATLAS-X polypeptide of species other than humans, including, but not limited to, mammals, and thus can include, *e.g.*, mouse, rat, rabbit, dog, cat cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the nucleotide sequence encoding human ATLAS-X protein. Homologous nucleic acid sequences include those nucleic acid sequences that encode

conservative amino acid substitutions (see below) in SEQ ID NO:1, 3, 5, or 7, as well as a polypeptide having ATLAS-X activity. Biological activities of the ATLAS-X proteins are described below. A homologous amino acid sequence does not encode the amino acid sequence of a human ATLAS-X polypeptide.

An ATLAS-X polypeptide is encoded by the open reading frame ("ORF") of an ATLAS-X nucleic acid. The invention includes the nucleic acid sequence comprising the stretch of nucleic acid sequences of SEQ ID NOs:1, 3, 5, 7, 9, 10, 11, or 12 that comprises the ORF of that nucleic acid sequence and encodes a polypeptide of SEQ ID NOs:2, 4, 6, or 8.

An "open reading frame" ("ORF") corresponds to a nucleotide sequence that could potentially be translated into a polypeptide. A stretch of nucleic acids comprising an ORF is uninterrupted by a stop codon. An ORF that represents the coding sequence for a full protein begins with an ATG "start" codon and terminates with one of the three "stop" codons, namely, TAA, TAG, or TGA. For the purposes of this invention, an ORF may be any part of a coding sequence, with or without a start codon, a stop codon, or both. For an ORF to be considered as a good candidate for coding for a bona fide cellular protein, a minimum size requirement is often set, for example, a stretch of DNA that would encode a protein of 50 amino acids or more.

The nucleotide sequence determined from the cloning of the human ATLAS-X gene allows for the generation of probes and primers designed for use in identifying and/or cloning ATLAS-X homologues in other cell types, *e.g.* from other tissues, as well as ATLAS-X homologues from other mammals. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 consecutive sense strand nucleotide sequence of SEQ ID NO:1, 3, 5, or 7, or an anti-sense strand nucleotide sequence of SEQ ID NO:1, 3, 5, or 7, or of a naturally occurring mutant of SEQ ID NO:1, 3, 5 or 7.

Probes based on the human ATLAS-X nucleotide sequence can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In various embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells or tissue which

misexpress an ATLAS-X protein, such as by measuring a level of an ATLAS-X-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting ATLAS-X mRNA levels or determining whether a genomic ATLAS-X gene has been mutated or deleted.

"A polypeptide having a biologically active portion of ATLAS-X" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. A nucleic acid fragment encoding a "biologically active portion of ATLAS-X" can be prepared by isolating a portion of SEQ ID NO:1, 3, 5, or 7 that encodes a polypeptide having an ATLAS-X biological activity (the biological activities of the ATLAS-X proteins are described below), expressing the encoded portion of ATLAS-X protein (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of ATLAS-X For example, a nucleic acid fragment can encode a biologically active portion of ATLAS-3 includes a thioredoxin domain of SEQ ID NO:6.

ATLAS-X variants

The invention further encompasses nucleic acid molecules that differ from the nucleotide sequence shown in SEQ ID NO:1, 3, 5, or 7 due to degeneracy of the genetic code and thus encode the same ATLAS-X protein as that encoded by the nucleotide sequence shown in SEQ ID NO:1, 3, 5, or 7. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in SEQ ID NO:2, 4, 6, or 8.

In addition to the human ATLAS-X nucleotide sequence shown in SEQ ID NO:1, 3, 5, 7, 9, 10, 11, or 12, it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of ATLAS-X may exist within a population (*e.g.*, the human population). Such genetic polymorphism in the ATLAS-X gene may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an ATLAS-X protein, preferably a mammalian ATLAS-X protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the ATLAS-X gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in ATLAS-X that are the result of natural allelic variation

and that do not alter the functional activity of ATLAS-X are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding ATLAS-X proteins from other species, and thus that have a nucleotide sequence that differs from the human sequence of SEQ ID NO:1, 3, 5, 7, 9, 10, 11, or 12 are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologues of the ATLAS-X cDNAs of the invention can be isolated based on their homology to the human ATLAS-X nucleic acids disclosed herein using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. For example, a soluble human ATLAS-X cDNA can be isolated based on its homology to human membrane-bound ATLAS-X. Likewise, a membrane-bound human ATLAS-X cDNA can be isolated based on its homology to soluble human ATLAS-X.

Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 6 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1, 3, 5, or 7. In another embodiment, the nucleic acid is at least 10, 25, 50, 100, 250, 500, 750, 1000, 1500, or 2000 or more nucleotides in length. In another embodiment, an isolated nucleic acid molecule of the invention hybridizes to the coding region. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other.

Homologs (*i.e.*, nucleic acids encoding ATLAS-X proteins derived from species other than human) or other related sequences (*e.g.*, paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

As used herein, the phrase "stringent hybridization conditions" refers to conditions under which a probe, primer or oligonucleotide will hybridize to its target sequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter sequences. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and pH. The Tm is the

temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at Tm, 50% of the probes are occupied at equilibrium. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes, primers or oligonucleotides (*e.g.*, 10 nt to 50 nt) and at least about 60°C for longer probes, primers and oligonucleotides. Stringent conditions may also be achieved with the addition of destabilizing agents, such as formamide.

Stringent conditions are known to those skilled in the art and can be found in Ausubel *et al.*, (eds.), CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. A non-limiting example of stringent hybridization conditions are hybridization in a high salt buffer comprising 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 mg/ml denatured salmon sperm DNA at 65°C, followed by one or more washes in 0.2X SSC, 0.01% BSA at 50°C. An isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequence of SEQ ID NO:1, 3, 5, or 7 corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein).

In a second embodiment, a nucleic acid sequence that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1, 3, 5, or 7 or fragments, analogs or derivatives thereof, under conditions of moderate stringency is provided. A non-limiting example of moderate stringency hybridization conditions are hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. Other conditions of moderate stringency that may be used are well-known in the art. See, *e.g.*, Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY.

In a third embodiment, a nucleic acid that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1, 3, 5, or 7 or fragments, analogs or derivatives thereof, under conditions of low stringency, is provided. A non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50°C. Other conditions of low stringency that may be used are well known in the art (*e.g.*, as employed for cross-species hybridizations). See, *e.g.*, Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY; Shilo and Weinberg, 1981, *Proc Natl Acad Sci USA 78*: 6789-6792.

Conservative mutations

In addition to naturally-occurring allelic variants of a ATLAS-X sequence that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequence of SEQ ID NO:1, 3, 5, or 7, thereby leading to changes in the amino acid sequence of the encoded ATLAS-X protein, without altering the functional ability of the ATLAS-X protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence of SEQ ID NO:1, 3, 5, or 7. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of ATLAS-X without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. For example, amino acid residues that are conserved among the ATLAS-X proteins of the present invention, are predicted to be particularly unamenable to alteration. Amino acids for which conservative substitutions can be made are known in the art.

Another aspect of the invention pertains to nucleic acid molecules encoding ATLAS-X proteins that contain changes in amino acid residues that are not essential for activity. Such ATLAS-X proteins differ in amino acid sequence from SEQ IDs NO:2, 4, 6, and 8, yet retain biological activity. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 45% homologous to the amino acid sequence of SEQ ID NO:2, 4, 6, or

8. Preferably, the protein encoded by the nucleic acid molecule is at least about 60% homologous to SEQ ID NO:2, 4, 6, or 8, more preferably at least about 70% homologous to SEQ ID NO:2, 4, 6, or 8, still more preferably at least about 80% homologous to SEQ ID NO:2, 4, 6, or 8, even more preferably at least about 90% homologous to SEQ ID NO:2, 4, 6, or 8, and most preferably at least about 95% homologous to SEQ ID NO:2, 4, 6, or 8.

An isolated nucleic acid molecule encoding an ATLAS-X protein homologous to the protein of SEQ ID NO:2, 4, 6, or 8 can be created by introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence of SEQ ID NO:2, 4, 6, or 8 such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein.

Mutations can be introduced into SEQ IDs NO:2, 4, 6, and 8 by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in ATLAS-X is replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an ATLAS-X coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for ATLAS-X biological activity to identify mutants that retain activity. Following mutagenesis of SEQ ID NO:2, 4, 6, or 8, the encoded protein can be expressed by any recombinant technology known in the art and the activity of the protein can be determined.

In one embodiment, a mutant ATLAS-X protein can be assayed for (1) the ability to form protein:protein interactions with other ATLAS-X proteins, other cell-surface proteins, or biologically active portions thereof, (2) complex formation between a mutant ATLAS-X

protein and an ATLAS-X ligand; (3) the ability of a mutant ATLAS-X protein to bind to an intracellular target protein or biologically active portion thereof; (*e.g.* avidin proteins).

In yet another embodiment, a mutant ATLAS-X can be assayed for the ability to regulate a phosphatase activity (for ATLAS-1), bind a cytokine (ATLAS-2), or act as a dithiol hydrogen donor (ATLAS-3).

Antisense

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire ATLAS-X coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of an ATLAS-X protein of SEQ ID NO:2, 4, 6, or 8, or antisense nucleic acids complementary to an ATLAS-X nucleic acid sequence of SEQ ID NO:1, 3, 5, or 7, are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding ATLAS-X. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the coding region of human ATLAS-1, 2, 3 and 4 correspond to SEQ IDs NO:9, 10, 11, and 12, respectively). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding ATLAS-X. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding ATLAS-X disclosed herein (*e.g.*, SEQ IDs NO:9, 10, 11 and 12), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of ATLAS-X mRNA, but more

preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of ATLAS-X mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of ATLAS-X mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an ATLAS-X protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense

nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient nucleic acid molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

Ribozymes and PNA moieties

Nucleic acid modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

In one embodiment, an antisense nucleic acid of the invention is a ribozyme.. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave ATLAS-X mRNA transcripts to thereby inhibit translation of ATLAS-X mRNA. A ribozyme having specificity for an ATLAS-X-encoding nucleic acid can be designed based upon the nucleotide sequence of an

ATLAS-X cDNA disclosed herein (*i.e.*, SEQ ID NO:1, 3, 5, 7, 9, 10, 11 or 12). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an ATLAS-X-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742. Alternatively, ATLAS-X mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, ATLAS-X gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the ATLAS-X (*e.g.*, the ATLAS-X promoter and/or enhancers) to form triple helical structures that prevent transcription of the ATLAS-X gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of ATLAS-X can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of ATLAS-X can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of ATLAS-X can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of ATLAS-X can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of ATLAS-X can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. WO88/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. WO89/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

ATLAS-X Polypeptides

A polypeptide according to the invention includes a polypeptide including the amino acid sequence of ATLAS-X polypeptides whose sequences are provided in Figures 1A-1D,

2A-2H, 3A-3B and 4A-4B (SEQ IDs NO:2, 4, 6, and 8). The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residues shown in Figures 1A-1D, 2A-2H, 3A-3B or 4A-4B while still encoding a protein that maintains its ATLAS-X activities and physiological functions, or a functional fragment thereof. In the mutant or variant protein, up to 20% or more of the residues may be so changed.

In general, an ATLAS-X variant that preserves ATLAS-X-like function includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further include the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above.

One aspect of the invention pertains to isolated ATLAS-X proteins, and biologically active portions thereof, or derivatives, fragments, analogs or homologs thereof. Also provided are polypeptide fragments suitable for use as immunogens to raise anti-ATLAS-X antibodies. In one embodiment, native ATLAS-X proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, ATLAS-X proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, an ATLAS-X protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" polypeptide or protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the ATLAS-X protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of ATLAS-X protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of ATLAS-X protein having less than about 30% (by dry weight) of non-ATLAS-X protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-ATLAS-X protein, still more preferably less than about 10% of

non-ATLAS-X protein, and most preferably less than about 5% non-ATLAS-X protein. When the ATLAS-X protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of ATLAS-X protein in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of ATLAS-X protein having less than about 30% (by dry weight) of chemical precursors or non-ATLAS-X chemicals, more preferably less than about 20% chemical precursors or non-ATLAS-X chemicals, still more preferably less than about 10% chemical precursors or non-ATLAS-X chemicals, and most preferably less than about 5% chemical precursors or non-ATLAS-X chemicals.

Biologically active portions of an ATLAS-X protein include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequence of the ATLAS-X protein, *e.g.*, the amino acid sequence shown in SEQ ID NO:2, 4, 5 or 8, that include fewer amino acids than the full length ATLAS-X proteins, and exhibit at least one activity of an ATLAS-X protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the ATLAS-X protein. A biologically active portion of an ATLAS-X protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length.

Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native ATLAS-X protein.

In an embodiment, the ATLAS-X protein has an amino acid sequence shown in SEQ ID NO:2, 4, 6 or 8. In other embodiments, the ATLAS-X protein is substantially homologous to SEQ ID NO:2, 4, 6 or 8 and retains the functional activity of the protein of SEQ ID NO:2, 4, 6 or 8 yet differs in amino acid sequence due to natural allelic variation or mutagenesis, as described in detail below. Accordingly, in another embodiment, the ATLAS-X protein is a protein that comprises an amino acid sequence at least about 45% homologous to the amino

acid sequence of SEQ ID NO:2, 4, 6 or 8 and retains the functional activity of the ATLAS-X proteins of SEQ ID NO:2, 4, 6 or 8.

Determining homol gy between two or more sequences

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity").

The nucleic acid sequence homology may be determined as the degree of identity between two sequences. The homology may be determined using computer programs known in the art, such as GAP software provided in the GCG program package. See, Needleman and Wunsch 1970 *J Mol Biol* 48: 443-453. Using GCG GAP software with the following settings for nucleic acid sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3, the coding region of the analogous nucleic acid sequences referred to above exhibits a degree of identity preferably of at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99%, with the CDS (encoding) part of the DNA sequence corresponding to nucleotides 1-2586 of SEQ ID NO:1, nucleotides 1-5553of SEQ ID NO:3, nucleotides 98-904 of SEQ ID NO:5, or nucleotides 1-1074 of SEQ ID NO:7.

The term "sequence identity" refers to the degree to which two polynucleotide or polypeptide sequences are identical on a residue-by-residue basis over a particular region of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, U, or I, in the case of nucleic acids) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The term "substantial identity" as used herein denotes a characteristic of a

polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 80 percent sequence identity, preferably at least 85 percent identity and often 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison region.

Chimeric and fusion proteins

The invention also provides ATLAS-X chimeric or fusion proteins. As used herein, an ATLAS-X "chimeric protein" or "fusion protein" comprises an ATLAS-X polypeptide operatively linked to a non-ATLAS-X polypeptide. An "ATLAS-X polypeptide" refers to a polypeptide having an amino acid sequence corresponding to ATLAS-X, whereas a "non-ATLAS-X polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the ATLAS-X protein, *e.g.*, a protein that is different from the ATLAS-X protein and that is derived from the same or a different organism. Within an ATLAS-X fusion protein the ATLAS-X polypeptide can correspond to all or a portion of an ATLAS-X protein. In one embodiment, an ATLAS-X fusion protein comprises at least one biologically active portion of an ATLAS-X protein. In another embodiment, an ATLAS-X fusion protein comprises at least two biologically active portions of an ATLAS-X protein. In yet another embodiment, an ATLAS-X fusion protein comprises at least three biologically active portions of an ATLAS-X protein. Within the fusion protein, the term "operatively linked" is intended to indicate that the ATLAS-X polypeptide and the non-ATLAS-X polypeptide are fused in-frame to each other. The non-ATLAS-X polypeptide can be fused to the N-terminus or C-terminus of the ATLAS-X polypeptide.

In one embodiment, the fusion protein is a GST-ATLAS-X fusion protein in which the ATLAS-X sequences are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences. Such fusion proteins can facilitate the purification of recombinant ATLAS-X.

In another embodiment, the fusion protein is an ATLAS-X protein containing a heterologous signal sequence at its N-terminus. For example, the native ATLAS-4 signal sequence (*i.e.*, about amino acids 1 to 28 of SEQ ID NO:8) can be removed and replaced with a signal sequence from another protein. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of ATLAS-X can be increased through use of a heterologous signal sequence.

In yet another embodiment, the fusion protein is an ATLAS-X-immunoglobulin fusion protein in which the ATLAS-X sequences are fused to sequences derived from a member of the immunoglobulin protein family. The ATLAS-X-immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between an ATLAS-X ligand and an ATLAS-X protein on the surface of a cell, to thereby suppress ATLAS-X-mediated signal transduction *in vivo*. The ATLAS-X-immunoglobulin fusion proteins can be used to affect the bioavailability of an ATLAS-X cognate ligand. Inhibition of the ATLAS-X ligand/ATLAS-X interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, as well as modulating (*e.g.* promoting or inhibiting) cell survival. Moreover, the ATLAS-X-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-ATLAS-X antibodies in a subject, to purify ATLAS-X ligands, and in screening assays to identify molecules that inhibit the interaction of ATLAS-X with an ATLAS-X ligand.

An ATLAS-X chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel *et al.* (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An ATLAS-X-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the ATLAS-X protein.

ATLAS-X agonists and antagonists

The present invention also pertains to variants of the ATLAS-X proteins that function as either ATLAS-X agonists (mimetics) or as ATLAS-X antagonists. Variants of the ATLAS-

X protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the ATLAS-X protein. An agonist of the ATLAS-X protein can retain substantially the same, or a subset of, the biological activities of the naturally occurring form of the ATLAS-X protein. An antagonist of the ATLAS-X protein can inhibit one or more of the activities of the naturally occurring form of the ATLAS-X protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the ATLAS-X protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. In one embodiment, treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein has fewer side effects in a subject relative to treatment with the naturally occurring form of the ATLAS-X proteins.

Variants of the ATLAS-X protein that function as either ATLAS-X agonists (mimetics) or as ATLAS-X antagonists can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the ATLAS-X protein for ATLAS-X protein agonist or antagonist activity. In one embodiment, a variegated library of ATLAS-X variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of ATLAS-X variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential ATLAS-X sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of ATLAS-X sequences therein. There are a variety of methods which can be used to produce libraries of potential ATLAS-X variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential ATLAS-X sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu Rev Biochem* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucl Acid Res* 11:477.

Polypeptide libraries

In addition, libraries of fragments of the ATLAS-X protein coding sequence can be used to generate a variegated population of ATLAS-X fragments for screening and subsequent

selection of variants of an ATLAS-X protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an ATLAS-X coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA that can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal and internal fragments of various sizes of the ATLAS-X protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of ATLAS-X proteins. The most widely used techniques, which are amenable to high throughput analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify ATLAS-X variants (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6:327-331).

Anti-ATLAS-X Antibodies

The invention encompasses antibodies and antibody fragments, such as F_{ab} or $(F_{ab})_2$, that bind immunospecifically to any of the polypeptides of the invention.

An isolated ATLAS-X protein, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that bind ATLAS-X using standard techniques for polyclonal and monoclonal antibody preparation. The full-length ATLAS-X protein can be used or, alternatively, the invention provides antigenic peptide fragments of ATLAS-X for use as immunogens. The antigenic peptide of ATLAS-X comprises at least 4 amino acid residues

of the amino acid sequence shown in SEQ ID NO:2, 4, 6, or 8 and encompasses an epitope of ATLAS-X such that an antibody raised against the peptide forms a specific immune complex with ATLAS-X. Preferably, the antigenic peptide comprises at least 6, 8, 10, 15, 20, or 30 amino acid residues. Longer antigenic peptides are sometimes preferable over shorter antigenic peptides, depending on use and according to methods well known to someone skilled in the art.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of ATLAS-X that is located on the surface of the protein, *e.g.*, a hydrophilic region. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each incorporated herein by reference in their entirety.

As disclosed herein, ATLAS-X protein sequence of SEQ ID NO:2, 4, 6,8, or derivatives, fragments, analogs or homologs thereof, may be utilized as immunogens in the generation of antibodies that immunospecifically-bind these protein components. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen, such as ATLAS-X. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} and $F_{(ab')2}$ fragments, and an F_{ab} expression library. In a specific embodiment, antibodies to human ATLAS-X proteins are disclosed. Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies to an ATLAS-X protein sequence of SEQ ID NO:2, 4, 6, 8, or a derivative, fragment, analog or homolog thereof. Some of these proteins are discussed below.

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by injection with the native protein, or a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, recombinantly expressed ATLAS-X protein or a chemically synthesized ATLAS-X polypeptide. The preparation can further include an

adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.); human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against ATLAS-X can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as protein A chromatography to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of ATLAS-X. A monoclonal antibody composition thus typically displays a single binding affinity for a particular ATLAS-X protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular ATLAS-X protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (see Kohler & Milstein, 1975 *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Each of the above citations is incorporated herein by reference in their entirety.

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an ATLAS-X protein (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methodscan be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, *et al.*, 1989 *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for an ATLAS-X protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See *e.g.*, U.S. Patent No. 5,225,539. Antibody fragments that

contain the idiotypes to an ATLAS-X protein may be produced by techniques known in the art including, but not limited to: (*i*) an $F_{(ab')2}$ fragment produced by pepsin digestion of an antibody molecule; (*ii*) an F_{ab} fragment generated by reducing the disulfide bridges of an $F_{(ab')2}$ fragment; (*iii*) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (*iv*) F_v fragments.

Additionally, recombinant anti-ATLAS-X antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Pat. No. 4,816,567; U.S. Pat. No. 5,225,539; European Patent Application No. 125,023; Better *et al.*(1988) *Science* 240:1041-1043; Liu *et al.* (1987) *PNAS* 84:3439-3443; Liu *et al.* (1987) *J Immunol.* 139:3521-3526; Sun *et al.* (1987) *PNAS* 84:214-218; Nishimura *et al.* (1987) *Cancer Res* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; Shaw *et al.* (1988) *J Natl Cancer Inst* 80:1553-1559); Morrison(1985) *Science* 229:1202-1207; Oi *et al.* (1986) *BioTechniques* 4:214; Jones *et al.* (1986) *Nature* 321:552-525; Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J Immunol* 141:4053-4060. Each of the above citations are incorporated herein by reference in their entirety.

In one embodiment, methods for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art. In a specific embodiment, selection of antibodies that are specific to a particular domain of an ATLAS-X protein is facilitated by generation of hybridomas that bind to the fragment of an ATLAS-X protein possessing such a domain. Thus, antibodies that are specific for a desired domain within an ATLAS-X protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

Anti-ATLAS-X antibodies may be used in methods known within the art relating to the localization and/or quantitation of an ATLAS-X protein (*e.g.*, for use in measuring levels of

the ATLAS-X protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for ATLAS-X proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody derived binding domain, are utilized as pharmacologically-active compounds [hereinafter "Therapeutics"].

An anti-ATLAS-X antibody (*e.g.*, monoclonal antibody) can be used to isolate ATLAS-X by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-ATLAS-X antibody can facilitate the purification of natural ATLAS-X from cells and of recombinantly produced ATLAS-X expressed in host cells. Moreover, an anti-ATLAS-X antibody can be used to detect ATLAS-X protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the ATLAS-X protein. Anti-ATLAS-X antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I, ^{131}I, ^{35}S or ^{3}H.

ATLAS-X Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding ATLAS-X protein, or derivatives, fragments, analogs or homologs thereof. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA

segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, that is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner that allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to includes promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, ATLAS-X proteins, mutant forms of ATLAS-X, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of ATLAS-X in prokaryotic or eukaryotic cells. For example, ATLAS-X can be expressed in bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: (1) to increase expression of recombinant protein; (2) to increase the solubility of the recombinant protein; and (3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5 (Pharmacia, Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann *et al.*, (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.*, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89).

One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein. See, Gottesman, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 119-128. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in *E. coli* (Wada *et al.*, (1992)

Nucleic Acids Res. 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the ATLAS-X expression vector is a yeast expression vector. Examples of vectors for expression in yeast S. cerivisae include pYepSec1 (Baldari, *et al.*, (1987) *EMBO J* 6:229-234), pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), pYES2 (Invitrogen Corporation, San Diego, Calif.), and picZ (InVitrogen Corp, San Diego, Calif.).

Alternatively, ATLAS-X can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, SF9 cells) include the pAc series (Smith *et al.* (1983) *Mol Cell Biol* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J* 6: 187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see, *e.g.*, Chapters 16 and 17 of Sambrook *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv Immunol* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*,

milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, *e.g.*, the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α-fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to ATLAS-X mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen that direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen that direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub *et al.*, "Antisense RNA as a molecular tool for genetic analysis," Reviews--Trends in Genetics, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, ATLAS-X protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and

"transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding ATLAS-X or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) ATLAS-X protein. Accordingly, the invention further provides methods for producing ATLAS-X protein using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding ATLAS-X has been introduced) in a suitable medium such that ATLAS-X protein is produced. In another embodiment, the method further comprises isolating ATLAS-X from the medium or the host cell.

Transgenic animals

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which ATLAS-X-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous ATLAS-X sequences have been introduced into their genome or homologous recombinant animals in which endogenous ATLAS-X sequences have been altered. Such animals are useful

for studying the function and/or activity of ATLAS-X and for identifying and/or evaluating modulators of ATLAS-X activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops and that remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous ATLAS-X gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing ATLAS-X-encoding nucleic acid into the male pronuclei of a fertilized oocyte, *e.g.*, by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. The human ATLAS-X cDNA sequence of SEQ ID NO:1, 3, 5, 7, 9, 10, 11, or 12 can be introduced as a transgene into the genome of a non-human animal. Alternatively, a nonhuman homologue of the human ATLAS-X gene, such as a mouse ATLAS-X gene, can be isolated based on hybridization to the human ATLAS-X cDNA (described further above) and used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to the ATLAS-X transgene to direct expression of ATLAS-X protein to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Pat. Nos. 4,736,866; 4,870,009; and 4,873,191; and Hogan 1986, In: MANIPULATING THE MOUSE EMBRYO, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the ATLAS-X transgene in its genome and/or expression of ATLAS-X mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals

carrying the transgene. Moreover, transgenic animals carrying a transgene encoding ATLAS-X can further be bred to other transgenic animals carrying other transgenes.

To create a homologous recombinant animal, a vector is prepared which contains at least a portion of an ATLAS-X gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the ATLAS-X gene. The ATLAS-X gene can be a human gene (*e.g.*, the cDNA of SEQ ID NO:1, 3, 5, or 7), but more preferably, is a non-human homologue of a human ATLAS-X gene. For example, a mouse homologue of human ATLAS-X gene of SEQ ID NO:1, 3, 5, or 7 can be used to construct a homologous recombination vector suitable for altering an endogenous ATLAS-X gene in the mouse genome. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous ATLAS-X gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector).

Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous ATLAS-X gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous ATLAS-X protein). In the homologous recombination vector, the altered portion of the ATLAS-X gene is flanked at its 5' and 3' ends by additional nucleic acid of the ATLAS-X gene to allow for homologous recombination to occur between the exogenous ATLAS-X gene carried by the vector and an endogenous ATLAS-X gene in an embryonic stem cell. The additional flanking ATLAS-X nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector. See *e.g.*, Thomas *et al.* (1987) *Cell* 51:503 for a description of homologous recombination vectors. The vector is introduced into an embryonic stem cell line (*e.g.*, by electroporation) and cells in which the introduced ATLAS-X gene has homologously recombined with the endogenous ATLAS-X gene are selected (see *e.g.*, Li *et al.* (1992) *Cell* 69:915).

The selected cells are then injected into a blastocyst of an animal (*e.g.*, a mouse) to form aggregation chimeras. See *e.g.*, Bradley 1987, In: TERATOCARCINOMAS AND EMBRYONIC STEM CELLS: A PRACTICAL APPROACH, Robertson, ed. IRL, Oxford, pp. 113-152. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously recombined DNA in their germ

cells can be used to breed animals in which all cells of the animal contain the homologously recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley (1991) *Curr Opin Biotechnol* 2:823-829; PCT International Publication Nos.: WO 90/11354; WO 91/01140; WO 92/0968; and WO 93/04169.

In another embodiment, transgenic non-humans animals can be produced that contain selected systems that allow for regulated expression of the transgene. One example of such a system is the cre/loxP recombinase system of bacteriophage P1. For a description of the cre/loxP recombinase system, see, *e.g.*, Lakso *et al.* (1992) *PNAS* 89:6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al.* (1991) *Science* 251:1351-1355. If a cre/loxP recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, *e.g.*, by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.* (1997) *Nature* 385:810-813. In brief, a cell, *e.g.*, a somatic cell, from the transgenic animal can be isolated and induced to exit the growth cycle and enter G_0 phase. The quiescent cell can then be fused, *e.g.*, through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or blastocyte and then transferred to pseudopregnant female foster animal. The offspring borne of this female foster animal will be a clone of the animal from which the cell, *e.g.*, the somatic cell, is isolated.

Pharmaceutical Compositions

The ATLAS-X nucleic acid molecules, ATLAS-X proteins, and anti-ATLAS-X antibodies (also referred to herein as "active compounds") of the invention, and derivatives, fragments, analogs and homologs thereof, can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein,

"pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Suitable carriers are described in the most recent edition of Remington's Pharmaceutical Sciences, a standard reference text in the field, which is incorporated herein by reference. Preferred examples of such carriers or diluents include, but are not limited to, water, saline, finger's solutions, dextrose solution, and 5% human serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringeability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion

medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, an ATLAS-X protein or anti-ATLAS-X antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation are vacuum drying and freeze-drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a

sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Pat. No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for

the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (see U.S. Pat. No. 5,328,470) or by stereotactic injection (see *e.g.*, Chen *et al.* (1994) *PNAS* 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

Uses and Methods of the Invention

The isolated nucleic acid molecules of the invention can be used to express ATLAS-X protein (*e.g.*, via a recombinant expression vector in a host cell in gene therapy applications), to detect ATLAS-X mRNA (*e.g.*, in a biological sample) or a genetic lesion in an ATLAS-X gene, and to modulate ATLAS-X activity, as described further below. In addition, the ATLAS-X proteins can be used to screen drugs or compounds that modulate the ATLAS-X activity or expression as well as to treat disorders characterized by insufficient or excessive production of ATLAS-X protein or production of ATLAS-X protein forms that have decreased or aberrant activity compared to ATLAS-X wild type protein (*e.g.* proliferative disorders such as cancer and immune disorders, *e.g.*, multiple sclerosis. In addition, the anti-ATLAS-X antibodies of the invention can be used to detect and isolate ATLAS-X proteins and modulate ATLAS-X activity.

This invention further pertains to novel agents identified by the screening assays described herein and uses thereof for treatments as described herein.

Screening Assays

The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides, peptidomimetics, small molecules or other drugs) that bind to ATLAS-X proteins or have a stimulatory or inhibitory effect on, for example, ATLAS-X expression or ATLAS-X activity. The invention also includes compounds identified in the screening assays described herein.

In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of the membrane-bound form of an ATLAS-X protein or polypeptide or biologically active portion thereof. The test compounds of the present invention can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam (1997) *Anticancer Drug Des* 12:145).

A "small molecule" as used herein, is meant to refer to a composition that has a molecular weight of less than about 5 kD and most preferably less than about 4 kD. Small molecules can be, *e.g.*, nucleic acids, peptides, polypeptides, peptidomimetics, carbohydrates, lipids or other organic (carbon containing) or inorganic molecules. Libraries of chemical and/or biological mixtures, such as fungal, bacterial, or algal extracts, are known in the art and can be screened with any of the assays of the invention.

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc Natl Acad Sci U.S.A.* 90:6909; Erb *et al.* (1994) *Proc Natl Acad Sci U.S.A.* 91:11422; Zuckermann *et al.* (1994) *J Med Chem* 37:2678; Cho *et al.* (1993) *Science* 261:1303; Carrell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2059; Carell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2061; and Gallop *et al.* (1994) *J Med Chem* 37:1233.

Libraries of compounds may be presented in solution (*e.g.*, Houghten (1992) *Biotechniques* 13:412-421), or on beads (Lam (1991) *Nature* 354:82-84), on chips (Fodor (1993) *Nature* 364:555-556), bacteria (Ladner U.S. Pat. No. 5,223,409), spores (Ladner USP '409), plasmids (Cull *et al.* (1992) *Proc Natl Acad Sci USA* 89:1865-1869) or on phage (Scott

and Smith (1990) *Science* 249:386-390; Devlin (1990) *Science* 249:404-406; Cwirla *et al.* (1990) *Proc Natl Acad Sci U.S.A.* 87:6378-6382; Felici (1991) *J Mol Biol* 222:301-310; Ladner above.).

In one embodiment, an assay is a cell-based assay in which a cell which expresses a membrane-bound form of ATLAS-X protein, or a biologically active portion thereof, on the cell surface is contacted with a test compound and the ability of the test compound to bind to an ATLAS-X protein determined. The cell, for example, can of mammalian origin or a yeast cell. Determining the ability of the test compound to bind to the ATLAS-X protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the ATLAS-X protein or biologically active portion thereof can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with ^{125}I, ^{35}S, ^{14}C, or ^{3}H, either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test compounds can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In one embodiment, the assay comprises contacting a cell which expresses a membrane-bound form of ATLAS-X protein, or a biologically active portion thereof, on the cell surface with a known compound which binds ATLAS-X to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an ATLAS-X protein, wherein determining the ability of the test compound to interact with an ATLAS-X protein comprises determining the ability of the test compound to preferentially bind to ATLAS-X or a biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of ATLAS-X protein, or a biologically active portion thereof, on the cell surface with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ATLAS-X protein or biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ATLAS-X or a biologically active portion thereof can be accomplished, for example, by determining the ability of the ATLAS-X protein to bind to or interact with an ATLAS-X target molecule. As used herein, a "target molecule" is a molecule with which an ATLAS-X protein binds or interacts in nature, for example, a molecule on the surface of a cell

which expresses an ATLAS-X interacting protein, a molecule on the surface of a second cell, a molecule in the extracellular milieu, a molecule associated with the internal surface of a cell membrane or a cytoplasmic molecule. An ATLAS-X target molecule can be a non-ATLAS-X molecule or an ATLAS-X protein or polypeptide of the present invention. In one embodiment, an ATLAS-X target molecule is a component of a signal transduction pathway that facilitates transduction of an extracellular signal (*e.g.* a signal generated by binding of a compound to a membrane-bound ATLAS-X molecule) through the cell membrane and into the cell. The target, for example, can be a second intercellular protein that has catalytic activity or a protein that facilitates the association of downstream signaling molecules with ATLAS-X.

Determining the ability of the ATLAS-X protein to bind to or interact with an ATLAS-X target molecule can be accomplished by one of the methods described above for determining direct binding. In one embodiment, determining the ability of the ATLAS-X protein to bind to or interact with an ATLAS-X target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (*i.e.* intracellular Ca^{2+}, diacylglycerol, IP_3, etc.), detecting catalytic/enzymatic activity of the target an appropriate substrate, detecting the induction of a reporter gene (comprising an ATLAS-X-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, *e.g.*, luciferase), or detecting a cellular response, for example, cell survival, cellular differentiation, or cell proliferation.

In yet another embodiment, an assay of the present invention is a cell-free assay comprising contacting an ATLAS-X protein or biologically active portion thereof with a test compound and determining the ability of the test compound to bind to the ATLAS-X protein or biologically active portion thereof. Binding of the test compound to the ATLAS-X protein can be determined either directly or indirectly as described above. In one embodiment, the assay comprises contacting the ATLAS-X protein or biologically active portion thereof with a known compound which binds ATLAS-X to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an ATLAS-X protein, wherein determining the ability of the test compound to interact with an ATLAS-X protein comprises determining the ability of the test compound to preferentially bind to ATLAS-X or biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-free assay comprising contacting ATLAS-X protein or biologically active portion thereof with a test compound and determining the ability of the test compound to modulate (*e.g.* stimulate or inhibit) the activity of the ATLAS-X protein or biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ATLAS-X can be accomplished, for example, by determining the ability of the ATLAS-X protein to bind to an ATLAS-X target molecule by one of the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of ATLAS-X can be accomplished by determining the ability of the ATLAS-X protein further modulate an ATLAS-X target molecule. For example, the catalytic/enzymatic activity of the target molecule on an appropriate substrate can be determined as previously described.

In yet another embodiment, the cell-free assay comprises contacting the ATLAS-X protein or biologically active portion thereof with a known compound which binds ATLAS-X to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an ATLAS-X protein, wherein determining the ability of the test compound to interact with an ATLAS-X protein comprises determining the ability of the ATLAS-X protein to preferentially bind to or modulate the activity of an ATLAS-X target molecule.

The cell-free assays of the present invention are amenable to use of both the soluble form or the membrane-bound form of ATLAS-X. In the case of cell-free assays comprising the membrane-bound form of ATLAS-X, it may be desirable to utilize a solubilizing agent such that the membrane-bound form of ATLAS-X is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton® X-100, Triton® X-114, Thesit®, Isotridecypoly(ethylene glycol ether)$_n$, N-dodecyl--N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl)dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either ATLAS-X or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to

accommodate automation of the assay. Binding of a test compound to ATLAS-X, or interaction of ATLAS-X with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For example, GST-ATLAS-X fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, that are then combined with the test compound or the test compound and either the non-adsorbed target protein or ATLAS-X protein, and the mixture is incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of ATLAS-X binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either ATLAS-X or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated ATLAS-X or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with ATLAS-X or target molecules, but which do not interfere with binding of the ATLAS-X protein to its target molecule, can be derivatized to the wells of the plate, and unbound target or ATLAS-X trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the ATLAS-X or target molecule, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the ATLAS-X or target molecule.

In another embodiment, modulators of ATLAS-X expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of ATLAS-X mRNA or protein in the cell is determined. The level of expression of ATLAS-X mRNA or protein in the presence of the candidate compound is compared to the level of expression of

ATLAS-X mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of ATLAS-X expression based on this comparison. For example, when expression of ATLAS-X mRNA or protein is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of ATLAS-X mRNA or protein expression. Alternatively, when expression of ATLAS-X mRNA or protein is less (statistically significantly less) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of ATLAS-X mRNA or protein expression. The level of ATLAS-X mRNA or protein expression in the cells can be determined by methods described herein for detecting ATLAS-X mRNA or protein.

In yet another aspect of the invention, the ATLAS-X proteins can be used as "bait proteins" in a two-hybrid assay or three hybrid assay (see, *e.g.*, U.S. Pat. No. 5,283,317; Zervos *et al.* (1993) Cell 72:223-232; Madura *et al.* (1993) J Biol Chem 268:12046-12054; Bartel *et al.* (1993) Biotechniques 14:920-924; Iwabuchi *et al.* (1993) Oncogene 8:1693-1696; and Brent WO94/10300), to identify other proteins that bind to or interact with ATLAS-X ("ATLAS-X-binding proteins" or "ATLAS-X-bp") and modulate ATLAS-X activity. Such ATLAS-X-binding proteins are also likely to be involved in the propagation of signals by the ATLAS-X proteins as, for example, upstream or downstream elements of the ATLAS-X pathway.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for ATLAS-X is fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming an ATLAS-X-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) that is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the protein which interacts with ATLAS-X.

This invention further pertains to novel agents identified by the above-described screening assays and uses thereof for treatments as described herein.

Detection Assays

Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For example, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; and (ii) identify an individual from a minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample. Some of these applications are described in the subsections below.

Chromosome Mapping

Once the sequence (or a portion of the sequence) of a gene has been isolated, this sequence can be used to map the location of the gene on a chromosome. This process is called chromosome mapping. Accordingly, portions or fragments of the ATLAS-X, sequences, described herein, can be used to map the location of the ATLAS-X genes, respectively, on a chromosome. The mapping of the ATLAS-X sequences to chromosomes is an important first step in correlating these sequences with genes associated with disease.

Briefly, ATLAS-X genes can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp in length) from the ATLAS-X sequences. Computer analysis of the ATLAS-X, sequences can be used to rapidly select primers that do not span more than one exon in the genomic DNA, thus complicating the amplification process. These primers can then be used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the ATLAS-X sequences will yield an amplified fragment.

Somatic cell hybrids are prepared by fusing somatic cells from different mammals (*e.g.*, human and mouse cells). As hybrids of human and mouse cells grow and divide, they gradually lose human chromosomes in random order, but retain the mouse chromosomes. By using media in which mouse cells cannot grow, because they lack a particular enzyme, but in which human cells can, the one human chromosome that contains the gene encoding the needed enzyme will be retained. By using various media, panels of hybrid cell lines can be established. Each cell line in a panel contains either a single human chromosome or a small

number of human chromosomes, and a full set of mouse chromosomes, allowing easy mapping of individual genes to specific human chromosomes. (D'Eustachio *et al.* (1983) *Science* 220:919-924). Somatic cell hybrids containing only fragments of human chromosomes can also be produced by using human chromosomes with translocations and deletions.

PCR mapping of somatic cell hybrids is a rapid procedure for assigning a particular sequence to a particular chromosome. Three or more sequences can be assigned per day using a single thermal cycler. Using the ATLAS-X sequences to design oligonucleotide primers, sublocalization can be achieved with panels of fragments from specific chromosomes.

Fluorescence *in situ* hybridization (FISH) of a DNA sequence to a metaphase chromosomal spread can further be used to provide a precise chromosomal location in one step. Chromosome spreads can be made using cells whose division has been blocked in metaphase by a chemical like colcemid that disrupts the mitotic spindle. The chromosomes can be treated briefly with trypsin, and then stained with Giemsa. A pattern of light and dark bands develops on each chromosome, so that the chromosomes can be identified individually. The FISH technique can be used with a DNA sequence as short as 500 or 600 bases. However, clones larger than 1,000 bases have a higher likelihood of binding to a unique chromosomal location with sufficient signal intensity for simple detection. Preferably 1,000 bases, and more preferably 2,000 bases, will suffice to get good results at a reasonable amount of time. For a review of this technique, see Verma *et al.*, HUMAN CHROMOSOMES: A MANUAL OF BASIC TECHNIQUES (Pergamon Press, New York 1988).

Reagents for chromosome mapping can be used individually to mark a single chromosome or a single site on that chromosome, or panels of reagents can be used for marking multiple sites and/or multiple chromosomes. Reagents corresponding to noncoding regions of the genes actually are preferred for mapping purposes. Coding sequences are more likely to be conserved within gene families, thus increasing the chance of cross hybridizations during chromosomal mapping.

Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. Such data are found, for example, in McKusick, MENDELIAN INHERITANCE IN MAN, available on-line through Johns Hopkins University Welch Medical Library). The relationship between genes and disease, mapped to the same chromosomal region, can then be identified through

linkage analysis (co-inheritance of physically adjacent genes), described in, for example, Egeland *et al.* (1987) *Nature*, 325:783-787.

Moreover, differences in the DNA sequences between individuals affected and unaffected with a disease associated with the ATLAS-X gene, can be determined. If a mutation is observed in some or all of the affected individuals but not in any unaffected individuals, then the mutation is likely to be the causative agent of the particular disease. Comparison of affected and unaffected individuals generally involves first looking for structural alterations in the chromosomes, such as deletions or translocations that are visible from chromosome spreads or detectable using PCR based on that DNA sequence. Ultimately, complete sequencing of genes from several individuals can be performed to confirm the presence of a mutation and to distinguish mutations from polymorphisms.

Tissue Typing

The ATLAS-X sequences of the present invention can also be used to identify individuals from minute biological samples. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identification. The sequences of the present invention are useful as additional DNA markers for RFLP ("restriction fragment length polymorphisms," described in U.S. Pat. No. 5,272,057).

Furthermore, the sequences of the present invention can be used to provide an alternative technique that determines the actual base-by-base DNA sequence of selected portions of an individual's genome. Thus, the ATLAS-X sequences described herein can be used to prepare two PCR primers from the 5' and 3' ends of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it.

Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have a unique set of such DNA sequences due to allelic differences. The sequences of the present invention can be used to obtain such identification sequences from individuals and from tissue. The ATLAS-X sequences of the invention uniquely represent portions of the human genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. It is estimated that allelic variation between individual humans occurs with a frequency of about once per each 500 bases. Much of the allelic variation is due to single

nucleotide polymorphisms (SNPs), which include restriction fragment length polymorphisms (RFLPs).

Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in the noncoding regions, fewer sequences are necessary to differentiate individuals. The noncoding sequences of SEQ ID NO:1, 3, 5 or 7 can comfortably provide positive individual identification with a panel of perhaps 10 to 1,000 primers that each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences, such as those in nucleotides 1-2586 of SEQ ID NO:1, nucleotides 1-5553of SEQ ID NO:3, nucleotides 98-904 of SEQ ID NO:5, or nucleotides 1-1074 of SEQ ID NO:7.are used, a more appropriate number of primers for positive individual identification would be 500-2,000.

Predictive Medicine

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ATLAS-X protein and/or nucleic acid expression as well as ATLAS-X activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ATLAS-X expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ATLAS-X protein, nucleic acid expression or activity. For example, mutations in an ATLAS-X gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ATLAS-X protein, nucleic acid expression or activity.

Another aspect of the invention provides methods for determining ATLAS-X protein, nucleic acid expression or ATLAS-X activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for

therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ATLAS-X in clinical trials.

These and other agents are described in further detail in the following sections.

Diagnostic Assays

An exemplary method for detecting the presence or absence of ATLAS-X in a biological sample involves obtaining a biological sample from a test subject and contacting the biological sample with a compound or an agent capable of detecting ATLAS-X protein or nucleic acid (*e.g.*, mRNA, genomic DNA) that encodes ATLAS-X protein such that the presence of ATLAS-X is detected in the biological sample. An agent for detecting ATLAS-X mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to ATLAS-X mRNA or genomic DNA. The nucleic acid probe can be, for example, a full-length ATLAS-X nucleic acid, such as the nucleic acid of SEQ ID NO:1, 3, 5, 7, or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to ATLAS-X mRNA or genomic DNA. Other suitable probes for use in the diagnostic assays of the invention are described herein.

An agent for detecting ATLAS-X protein is an antibody capable of binding to ATLAS-X protein, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or $F(ab')_2$) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin. The term "biological sample" is intended to include tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject. That is, the detection method of the invention can be used to detect ATLAS-X mRNA, protein, or genomic DNA in a biological sample *in vitro* as well as *in vivo*. For

example, *in vitro* techniques for detection of ATLAS-X mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of ATLAS-X protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. *In vitro* techniques for detection of ATLAS-X genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of ATLAS-X protein include introducing into a subject a labeled anti-ATLAS-X antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample contains protein molecules from the test subject. Alternatively, the biological sample can contain mRNA molecules from the test subject or genomic DNA molecules from the test subject. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject.

In another embodiment, the methods further involve obtaining a control biological sample from a control subject, contacting the control sample with a compound or agent capable of detecting ATLAS-X protein, mRNA, or genomic DNA, such that the presence of ATLAS-X protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of ATLAS-X protein, mRNA or genomic DNA in the control sample with the presence of ATLAS-X protein, mRNA or genomic DNA in the test sample.

The invention also encompasses kits for detecting the presence of ATLAS-X in a biological sample. For example, the kit can comprise: a labeled compound or agent capable of detecting ATLAS-X protein or mRNA in a biological sample; means for determining the amount of ATLAS-X in the sample; and means for comparing the amount of ATLAS-X in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect ATLAS-X protein or nucleic acid.

Prognostic Assays

The diagnostic methods described herein can furthermore be utilized to identify subjects having or at risk of developing a disease or disorder associated with aberrant ATLAS-X expression or activity. For example, the assays described herein, such as the preceding diagnostic assays or the following assays, can be utilized to identify a subject having or at risk of developing a disorder associated with ATLAS-X protein, nucleic acid expression or activity

such as cancer, immune system associated (*e.g.*, multiple sclerosis), or fibrotic disorders.. Alternatively, the prognostic assays can be utilized to identify a subject having or at risk for developing a disease or disorder. Thus, the present invention provides a method for identifying a disease or disorder associated with aberrant ATLAS-X expression or activity in which a test sample is obtained from a subject and ATLAS-X protein or nucleic acid (*e.g.*, mRNA, genomic DNA) is detected, wherein the presence of ATLAS-X protein or nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant ATLAS-X expression or activity. As used herein, a "test sample" refers to a biological sample obtained from a subject of interest. For example, a test sample can be a biological fluid (*e.g.*, serum), cell sample, or tissue.

Furthermore, the prognostic assays described herein can be used to determine whether a subject can be administered an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder associated with aberrant ATLAS-X expression or activity. For example, such methods can be used to determine whether a subject can be effectively treated with an agent for a disorder, such as cancer, immune system associated disorders, *e.g.*, multiple sclerosis. Thus, the present invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with aberrant ATLAS-X expression or activity in which a test sample is obtained and ATLAS-X protein or nucleic acid is detected (*e.g.*, wherein the presence of ATLAS-X protein or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with aberrant ATLAS-X expression or activity.)

The methods of the invention can also be used to detect genetic lesions in an ATLAS-X gene, thereby determining if a subject with the lesioned gene is at risk for a disorder characterized by aberrant cell proliferation and/or differentiation. In various embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic lesion characterized by at least one of an alteration affecting the integrity of a gene encoding an ATLAS-X-protein, or the mis-expression of the ATLAS-X gene. For example, such genetic lesions can be detected by ascertaining the existence of at least one of (1) a deletion of one or more nucleotides from an ATLAS-X gene; (2) an addition of one or more nucleotides to an ATLAS-X gene; (3) a substitution of one or more nucleotides of an ATLAS-X gene, (4) a chromosomal rearrangement of an ATLAS-X gene; (5) an alteration in the level

of a messenger RNA transcript of an ATLAS-X gene, (6) aberrant modification of an ATLAS-X gene, such as of the methylation pattern of the genomic DNA, (7) the presence of a non-wild type splicing pattern of a messenger RNA transcript of an ATLAS-X gene, (8) a non-wild type level of an ATLAS-X-protein, (9) allelic loss of an ATLAS-X gene, and (10) inappropriate post-translational modification of an ATLAS-X-protein. As described herein, there are a large number of assay techniques known in the art which can be used for detecting lesions in an ATLAS-X gene. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

In certain embodiments, detection of the lesion involves the use of a probe/primer in a polymerase chain reaction (PCR) (see, *e.g.*, U.S. Pat. Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (see, *e.g.*, Landegran *et al.* (1988) *Science* 241:1077-1080; and Nakazawa *et al.* (1994) *PNAS* 91:360-364), the latter of which can be particularly useful for detecting point mutations in the ATLAS-X-gene (see Abravaya *et al.* (1995) *Nucl Acids Res* 23:675-682). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (*e.g.*, genomic, mRNA or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers that specifically hybridize to an ATLAS-X gene under conditions such that hybridization and amplification of the ATLAS-X gene (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (Guatelli *et al.*, 1990, *Proc Natl Acad Sci USA* 87:1874-1878), transcriptional amplification system (Kwoh, *et al.*, 1989, *Proc Natl Acad Sci USA* 86:1173-1177), Q-Beta Replicase (Lizardi *et al*, 1988, *BioTechnology* 6:1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

In an alternative embodiment, mutations in an ATLAS-X gene from a sample cell can be identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared. Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (see, for example, U.S. Pat. No. 5,493,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

In other embodiments, genetic mutations in ATLAS-X can be identified by hybridizing a sample and control nucleic acids, *e.g.*, DNA or RNA, to high density arrays containing hundreds or thousands of oligonucleotides probes (Cronin *et al.* (1996) *Human Mutation* 7: 244-255; Kozal *et al.* (1996) *Nature Medicine* 2: 753-759). For example, genetic mutations in ATLAS-X can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin *et al.* above. Briefly, a first hybridization array of probes can be used to scan through long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This step is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the ATLAS-X gene and detect mutations by comparing the sequence of the sample ATLAS-X with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on techniques developed by Maxim and Gilbert (1977) *PNAS* 74:560 or Sanger (1977) *PNAS* 74:5463. It is also contemplated that any of a variety of automated sequencing procedures can be utilized when performing the diagnostic assays (Naeve *et al.*, (1995) *Biotechniques* 19:448), including sequencing by mass spectrometry (see, *e.g.*, PCT International Publ. No. WO 94/16101; Cohen *et al.* (1996) *Adv Chromatogr* 36:127-162; and Griffin *et al.* (1993) *Appl Biochem Biotechnol* 38:147-159).

Other methods for detecting mutations in the ATLAS-X gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA heteroduplexes (Myers *et al.* (1985) *Science* 230:1242). In general, the art technique of "mismatch cleavage" starts by providing heteroduplexes of formed by hybridizing (labeled) RNA or DNA containing the wild-type ATLAS-X sequence with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent that cleaves single-stranded regions of the duplex such as which will exist due to basepair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S1 nuclease to enzymatically digesting the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of mutation. See, for example, Cotton *et al* (1988) *Proc Natl Acad Sci USA* 85:4397; Saleeba *et al* (1992) *Methods Enzymol* 217:286-295. In an embodiment, the control DNA or RNA can be labeled for detection.

In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in ATLAS-X cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches (Hsu *et al.* (1994) *Carcinogenesis* 15:1657-1662). According to an exemplary embodiment, a probe based on an ATLAS-X sequence, *e.g.*, a wild-type ATLAS-X sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like. See, for example, U.S. Pat. No. 5,459,039.

In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in ATLAS-X genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Orita *et al.* (1989) *Proc Natl Acad Sci USA*: 86:2766, see also Cotton (1993) *Mutat Res* 285:125-144; Hayashi (1992) *Genet Anal Tech Appl* 9:73-79). Single-stranded DNA fragments of sample and control ATLAS-X nucleic acids will be

denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a change in sequence. In one embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility (Keen *et al.* (1991) *Trends Genet* 7:5).

In yet another embodiment the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE) (Myers *et al* (1985) *Nature* 313:495). When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA (Rosenbaum and Reissner (1987) *Biophys Chem* 265:12753).

Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions that permit hybridization only if a perfect match is found (Saiki *et al.* (1986) *Nature* 324:163); Saiki *et al.* (1989) *Proc Natl Acad. Sci USA* 86:6230). Such allele specific oligonucleotides are hybridized to PCR amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization) (Gibbs *et al.* (1989) *Nucleic Acids Res* 17:2437-2448) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prossner (1993) *Tibtech* 11:238). In addition it may be desirable to introduce a novel restriction site in

the region of the mutation to create cleavage-based detection (Gasparini *et al* (1992) *Mol Cell Probes* 6:1). It is anticipated that in certain embodiments amplification may also be performed using Taq ligase for amplification (Barany (1991) *Proc Natl Acad Sci USA* 88:189). In such cases, ligation will occur only if there is a perfect match at the 3' end of the 5' sequence, making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, *e.g.*, in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving an ATLAS-X gene.

Furthermore, any cell type or tissue, preferably peripheral blood leukocytes, in which ATLAS-X is expressed may be utilized in the prognostic assays described herein. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

Pharmacogenomics

Agents, or modulators that have a stimulatory or inhibitory effect on ATLAS-X activity (*e.g.*, ATLAS-X gene expression), as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) disorders (*e.g.*, cancer or immune disorders associated with aberrant ATLAS-X activity. In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate dosages and therapeutic regimens. Accordingly, the activity of ATLAS-X protein, expression of ATLAS-X nucleic acid, or mutation content of ATLAS-X genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See *e.g.*, Eichelbaum, *Clin Exp Pharmacol Physiol*, 1996, 23:983-985 and Linder, *Clin Chem*, 1997, 43:254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is haemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. At the other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the activity of ATLAS-X protein, expression of ATLAS-X nucleic acid, or mutation content of ATLAS-X genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness

phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with an ATLAS-X modulator, such as a modulator identified by one of the exemplary screening assays described herein.

Monitoring of Effects During Clinical Trials

Monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ATLAS-X (*e.g.*, the ability to modulate aberrant cell proliferation and/or differentiation) can be applied not only in basic drug screening, but also in clinical trials. For example, the effectiveness of an agent determined by a screening assay as described herein to increase ATLAS-X gene expression, protein levels, or upregulate ATLAS-X activity, can be monitored in clinical trails of subjects exhibiting decreased ATLAS-X gene expression, protein levels, or downregulated ATLAS-X activity. Alternatively, the effectiveness of an agent determined by a screening assay to decrease ATLAS-X gene expression, protein levels, or downregulate ATLAS-X activity, can be monitored in clinical trails of subjects exhibiting increased ATLAS-X gene expression, protein levels, or upregulated ATLAS-X activity. In such clinical trials, the expression or activity of ATLAS-X and, preferably, other genes that have been implicated in, for example, a cellular proliferation or immune disorder can be used as a "read out" or markers of the immune responsiveness of a particular cell.

For example, and not by way of limitation, genes, including ATLAS-X, that are modulated in cells by treatment with an agent (*e.g.*, compound, drug or small molecule) that modulates ATLAS-X activity (*e.g.*, identified in a screening assay as described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of ATLAS-X and other genes implicated in the disorder. The levels of gene expression (*i.e.*, a gene expression pattern) can be quantified by Northern blot analysis or RT-PCR, as described herein, or alternatively by measuring the amount of protein produced, by one of the methods as described herein, or by measuring the levels of activity of ATLAS-X or other genes. In this way, the gene expression pattern can serve as a marker, indicative of the physiological response of the cells to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the agent.

In one embodiment, the present invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, protein, peptide, peptidomimetic, nucleic acid, small molecule, or other drug candidate identified by the screening assays described herein) comprising the steps of (*i*) obtaining a pre-administration sample from a subject prior to administration of the agent; (*ii*) detecting the level of expression of an ATLAS-X protein, mRNA, or genomic DNA in the preadministration sample; (*iii*) obtaining one or more post-administration samples from the subject; (*iv*) detecting the level of expression or activity of the ATLAS-X protein, mRNA, or genomic DNA in the post-administration samples; (*v*) comparing the level of expression or activity of the ATLAS-X protein, mRNA, or genomic DNA in the pre-administration sample with the ATLAS-X protein, mRNA, or genomic DNA in the post administration sample or samples; and (*vi*) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of ATLAS-X to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of ATLAS-X to lower levels than detected, *i.e.*, to decrease the effectiveness of the agent.

Methods of Treatment

The present invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant ATLAS-X expression or activity.

Disorders

Diseases and disorders that are characterized by increased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that antagonize (*i.e.*, reduce or inhibit) activity. Therapeutics that antagonize activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to, (*i*) an aforementioned peptide, or analogs, derivatives, fragments or homologs thereof; (*ii*) antibodies to an aforementioned peptide; (*iii*) nucleic acids encoding an aforementioned peptide; (*iv*) administration of antisense nucleic acid and nucleic acids that are "dysfunctional" (*i.e.,* due to a heterologous insertion within the coding sequences of coding sequences to an aforementioned peptide) that are utilized to "knockout" endogenous function of an aforementioned peptide by homologous recombination

(see, *e.g.*, Capecchi, 1989, *Science* 244: 1288-1292); or (*v*) modulators (*i.e.*, inhibitors, agonists and antagonists, including additional peptide mimetic of the invention or antibodies specific to a peptide of the invention) that alter the interaction between an aforementioned peptide and its binding partner.

Diseases and disorders that are characterized by decreased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that increase (*i.e.*, are agonists to) activity. Therapeutics that upregulate activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to, an aforementioned peptide, or analogs, derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (*e.g.*, from biopsy tissue) and assaying it *in vitro* for RNA or peptide levels, structure and/or activity of the expressed peptides (or mRNAs of an aforementioned peptide). Methods that are well-known within the art include, but are not limited to, immunoassays (*e.g.*, by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis, immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs (*e.g.*, Northern assays, dot blots, *in situ* hybridization, etc.).

Prophylactic Methods

In one aspect, the invention provides a method for preventing, in a subject, a disease or condition associated with an aberrant ATLAS-X expression or activity, by administering to the subject an agent that modulates ATLAS-X expression or at least one ATLAS-X activity. Subjects at risk for a disease that is caused or contributed to by aberrant ATLAS-X expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the ATLAS-X aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending on the type of ATLAS-X aberrancy, for example, an ATLAS-X agonist or ATLAS-X antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein. The prophylactic methods of the present invention are further discussed in the following subsections.

Therapeutic Methods

Another aspect of the invention pertains to methods of modulating ATLAS-X expression or activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of ATLAS-X protein activity associated with the cell. An agent that modulates ATLAS-X protein activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring cognate ligand of an ATLAS-X protein, a peptide, an ATLAS-X peptidomimetic, or other small molecule. In one embodiment, the agent stimulates one or more ATLAS-X protein activity. Examples of such stimulatory agents include active ATLAS-X protein and a nucleic acid molecule encoding ATLAS-X that has been introduced into the cell. In another embodiment, the agent inhibits one or more ATLAS-X protein activity. Examples of such inhibitory agents include antisense ATLAS-X nucleic acid molecules and anti-ATLAS-X antibodies. These modulatory methods can be performed *in vitro* (*e.g.*, by culturing the cell with the agent) or, alternatively, *in vivo* (*e.g.*, by administering the agent to a subject). As such, the present invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of an ATLAS-X protein or nucleic acid molecule. In one embodiment, the method involves administering an agent (*e.g.*, an agent identified by a screening assay described herein), or combination of agents that modulates (*e.g.*, upregulates or downregulates) ATLAS-X expression or activity. In another embodiment, the method involves administering an ATLAS-X protein or nucleic acid molecule as therapy to compensate for reduced or aberrant ATLAS-X expression or activity.

Stimulation of ATLAS-X activity is desirable in situations in which ATLAS-X is abnormally downregulated and/or in which increased ATLAS-X activity is likely to have a beneficial effect. One example of such a situation is where a subject has a disorder characterized by aberrant cell proliferation and/or differentiation (*e.g.*, cancer or immune associated disorders). Another example of such a situation is where the subject has a gestational disease (*e.g.*, preclampsia).

Determination of the Biological Effect of the Therapeutic

In various embodiments of the present invention, suitable *in vitro* or *in vivo* assays are performed to determine the effect of a specific Therapeutic and whether its administration is indicated for treatment of the affected tissue.

In various specific embodiments, *in vitro* assays may be performed with representative cells of the type(s) involved in the patient's disorder, to determine if a given Therapeutic exerts the desired effect upon the cell type(s). Compounds for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly, for *in vivo* testing, any of the animal model system known in the art may be used prior to administration to human subjects.

Malignancies

Therapeutics of the present invention may be useful in the therapeutic or prophylactic treatment of diseases or disorders that are associated with cell hyperproliferation and/or loss of control of cell proliferation (*e.g.*, cancers, malignancies and tumors). For a review of such hyperproliferation disorders, see *e.g.*, Fishman, *et al.*, 1985. MEDICINE, 2nd ed., J.B. Lippincott Co., Philadelphia, PA.

Therapeutics of the present invention may be assayed by any method known within the art for efficacy in treating or preventing malignancies and related disorders. Such assays include, but are not limited to, *in vitro* assays utilizing transformed cells or cells derived from the patient's tumor, as well as *in vivo* assays using animal models of cancer or malignancies. Potentially effective Therapeutics are those that, for example, inhibit the proliferation of tumor-derived or transformed cells in culture or cause a regression of tumors in animal models, in comparison to the controls.

In the practice of the present invention, once a malignancy or cancer has been shown to be amenable to treatment by modulating (*i.e.*, inhibiting, antagonizing or agonizing) activity, that cancer or malignancy may subsequently be treated or prevented by the administration of a Therapeutic that serves to modulate protein function.

Premalignant conditions

The Therapeutics of the present invention that are effective in the therapeutic or prophylactic treatment of cancer or malignancies may also be administered for the treatment of pre-malignant conditions and/or to prevent the progression of a pre-malignancy to a neoplastic or malignant state. Such prophylactic or therapeutic use is indicated in conditions known or suspected of preceding progression to neoplasia or cancer, in particular, where non-neoplastic cell growth consisting of hyperplasia, metaplasia or, most particularly, dysplasia has occurred.

For a review of such abnormal cell growth see *e.g.*, Robbins & Angell, 1976. BASIC PATHOLOGY, 2nd ed., W.B. Saunders Co., Philadelphia, PA.

Hyperplasia is a form of controlled cell proliferation involving an increase in cell number in a tissue or organ, without significant alteration in its structure or function. For example, it has been demonstrated that endometrial hyperplasia often precedes endometrial cancer. Metaplasia is a form of controlled cell growth in which one type of mature or fully differentiated cell substitutes for another type of mature cell. Metaplasia may occur in epithelial or connective tissue cells. Dysplasia is generally considered a precursor of cancer, and is found mainly in the epithelia. Dysplasia is the most disorderly form of non-neoplastic cell growth, and involves a loss in individual cell uniformity and in the architectural orientation of cells. Dysplasia characteristically occurs where there exists chronic irritation or inflammation, and is often found in the cervix, respiratory passages, oral cavity, and gall bladder.

Alternatively, or in addition to the presence of abnormal cell growth characterized as hyperplasia, metaplasia, or dysplasia, the presence of one or more characteristics of a transformed or malignant phenotype displayed either *in vivo* or *in vitro* within a cell sample derived from a patient, is indicative of the desirability of prophylactic/therapeutic administration of a Therapeutic that possesses the ability to modulate activity of An aforementioned protein. Characteristics of a transformed phenotype include, but are not limited to: (*i*) morphological changes; (*ii*) looser substratum attachment; (*iii*) loss of cell-to-cell contact inhibition; (*iv*) loss of anchorage dependence; (*v*) protease release; (*vi*) increased sugar transport; (*vii*) decreased serum requirement; (*viii*) expression of fetal antigens, (*ix*) disappearance of the 250 kDal cell-surface protein, and the like. See *e.g.*, Richards, *et al.*, 1986. MOLECULAR PATHOLOGY, W.B. Saunders Co., Philadelphia, PA.

In a specific embodiment of the present invention, a patient that exhibits one or more of the following predisposing factors for malignancy is treated by administration of an effective amount of a Therapeutic: (*i*) a chromosomal translocation associated with a malignancy (*e.g.*, the Philadelphia chromosome (*bcr*/*abl*) for chronic myelogenous leukemia and t(14;18) for follicular lymphoma, etc.); (*ii*) familial polyposis or Gardner's syndrome (possible forerunners of colon cancer); (*iii*) monoclonal gammopathy of undetermined significance (a possible precursor of multiple myeloma) and (*iv*) a first degree kinship with

persons having a cancer or pre-cancerous disease showing a Mendelian (genetic) inheritance pattern (*e.g.*, familial polyposis of the colon, Gardner's syndrome, hereditary exostosis, polyendocrine adenomatosis, Peutz-Jeghers syndrome, neurofibromatosis of Von Recklinghausen, medullary thyroid carcinoma with amyloid production and pheochromocytoma, retinoblastoma, carotid body tumor, cutaneous melanocarcinoma, intraocular melanocarcinoma, xeroderma pigmentosum, ataxia telangiectasia, Chediak-Higashi syndrome, albinism, Fanconi's aplastic anemia and Bloom's syndrome).

In another embodiment, a Therapeutic of the present invention is administered to a human patient to prevent the progression to breast, colon, lung, pancreatic, or uterine cancer, or melanoma or sarcoma.

Hyperproliferative and dysproliferative disorders

In one embodiment of the present invention, a Therapeutic is administered in the therapeutic or prophylactic treatment of hyperproliferative or benign dysproliferative disorders. The efficacy in treating or preventing hyperproliferative diseases or disorders of a Therapeutic of the present invention may be assayed by any method known within the art. Such assays include *in vitro* cell proliferation assays, *in vitro* or *in vivo* assays using animal models of hyperproliferative diseases or disorders, or the like. Potentially effective Therapeutics may, for example, promote cell proliferation in culture or cause growth or cell proliferation in animal models in comparison to controls.

Specific embodiments of the present invention are directed to the treatment or prevention of cirrhosis of the liver (a condition in which scarring has overtaken normal liver regeneration processes); treatment of keloid (hypertrophic scar) formation causing disfiguring of the skin in which the scarring process interferes with normal renewal; psoriasis (a common skin condition characterized by excessive proliferation of the skin and delay in proper cell fate determination); benign tumors; fibrocystic conditions and tissue hypertrophy (*e.g.*, benign prostatic hypertrophy).

Neurodegenerative disorders

ATLAS-X protein have been implicated in the deregulation of cellular maturation and apoptosis, which are both characteristic of neurodegenerative disease. Accordingly, Therapeutics of the invention, particularly but not limited to those that modulate (or supply) activity of an aforementioned protein, may be effective in treating or preventing

neurodegenerative disease. Therapeutics of the present invention that modulate the activity of an aforementioned protein involved in neurodegenerative disorders can be assayed by any method known in the art for efficacy in treating or preventing such neurodegenerative diseases and disorders. Such assays include *in vitro* assays for regulated cell maturation or inhibition of apoptosis or *in vivo* assays using animal models of neurodegenerative diseases or disorders, or any of the assays described below. Potentially effective Therapeutics, for example but not by way of limitation, promote regulated cell maturation and prevent cell apoptosis in culture, or reduce neurodegeneration in animal models in comparison to controls.

Once a neurodegenerative disease or disorder has been shown to be amenable to treatment by modulation activity, that neurodegenerative disease or disorder can be treated or prevented by administration of a Therapeutic that modulates activity. Such diseases include all degenerative disorders involved with aging, especially osteoarthritis and neurodegenerative disorders.

Disorders related to organ transplantation

ATLAS-X has been implicated in disorders related to organ transplantation, in particular but not limited to organ rejection. Therapeutics of the invention, particularly those that modulate (or supply) activity, may be effective in treating or preventing diseases or disorders related to organ transplantation. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity of an aforementioned protein) can be assayed by any method known in the art for efficacy in treating or preventing such diseases and disorders related to organ transplantation. Such assays include *in vitro* assays for using cell culture models as described below, or *in vivo* assays using animal models of diseases and disorders related to organ transplantation, see *e.g.*, below. Potentially effective Therapeutics, for example but not by way of limitation, reduce immune rejection responses in animal models in comparison to controls.

Accordingly, once diseases and disorders related to organ transplantation are shown to be amenable to treatment by modulation of activity, such diseases or disorders can be treated or prevented by administration of a Therapeutic that modulates activity.

Cardiovascular Disease

ATLAS-X has been implicated in cardiovascular disorders, including in atherosclerotic plaque formation. Diseases such as cardiovascular disease, including cerebral

thrombosis or hemorrhage, ischemic heart or renal disease, peripheral vascular disease, or thrombosis of other major vessel, and other diseases, including diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage disease, systemic lupus erythematosus, homocysteinemia, and familial protein or lipid processing diseases, and the like, are either directly or indirectly associated with atherosclerosis. Accordingly, Therapeutics of the invention, particularly those that modulate (or supply) activity or formation may be effective in treating or preventing atherosclerosis-associated diseases or disorders. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity) can be assayed by any method known in the art, including those described below, for efficacy in treating or preventing such diseases and disorders.

A vast array of animal and cell culture models exist for processes involved in atherosclerosis. A limited and non-exclusive list of animal models includes knockout mice for premature atherosclerosis (Kurabayashi and Yazaki, 1996, Int. Angiol. 15: 187-194), transgenic mouse models of atherosclerosis (Kappel *et al.*, 1994, FASEB J. 8: 583-592), antisense oligonucleotide treatment of animal models (Callow, 1995, Curr. Opin. Cardiol. 10: 569-576), transgenic rabbit models for atherosclerosis (Taylor, 1997, Ann. N.Y. Acad. Sci 811: 146-152), hypercholesterolemic animal models (Rosenfeld, 1996, Diabetes Res. Clin. Pract. 30 Suppl.: 1-11), hyperlipidemic mice (Paigen *et al.*, 1994, Curr. Opin. Lipidol. 5: 258-264), and inhibition of lipoxygenase in animals (Sigal *et al.*, 1994, Ann. N.Y. Acad. Sci. 714: 211-224). In addition, *in vitro* cell models include but are not limited to monocytes exposed to low density lipoprotein (Frostegard *et al.*, 1996, Atherosclerosis 121: 93-103), cloned vascular smooth muscle cells (Suttles *et al.*, 1995, Exp. Cell Res. 218: 331-338), endothelial cell-derived chemoattractant exposed T cells (Katz *et al.*, 1994, J. Leukoc. Biol. 55: 567-573), cultured human aortic endothelial cells (Farber *et al.*, 1992, Am. J. Physiol. 262: H1088-1085), and foam cell cultures (Libby *et al.*, 1996, Curr Opin Lipidol 7: 330-335). Potentially effective Therapeutics, for example but not by way of limitation, reduce foam cell formation in cell culture models, or reduce atherosclerotic plaque formation in hypercholesterolemic mouse models of atherosclerosis in comparison to controls.

Accordingly, once an atherosclerosis-associated disease or disorder has been shown to be amenable to treatment by modulation of activity or formation, that disease or disorder can be treated or prevented by administration of a Therapeutic that modulates activity.

Cytokine and Cell Proliferation/Differentiation Activity

An ATLAS-X protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods: Assays for T-cell or thymocyte proliferation include without limitation those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan *et al.*, Greene Publishing Associates and Wiley-Interscience (Chapter 3 and Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bertagnolli *et al.*, *J Immunol* 145:1706-1712, 1990; Bertagnolli *et al.*, *Cell Immunol* 133:327-341, 1991; Bertagnolli, *et al.*, *J Immunol* 149:3778-3783, 1992; Bowman *et al.*, *J Immunol* 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described by Kruisbeek and Shevach, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1, pp. 3.12.1-14, John Wiley and Sons, Toronto 1994; and by Schreiber, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan eds. Vol 1 pp. 6.8.1-8, John Wiley and Sons, Toronto 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described by Bottomly *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto 1991; deVries *et al.*, *J Exp Med* 173:1205-1211, 1991; Moreau *et al.*, *Nature* 336:690-692, 1988; Greenberger *et al.*, *Proc Natl Acad Sci U.S.A.* 80:2931-2938, 1983; Nordan, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.6.1-5, John Wiley and Sons, Toronto 1991; Smith *et al.*, *Proc Natl Acad Sci U.S.A.* 83:1857-1861, 1986; Measurement of human Interleukin 11-Bennett, *et* al. In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto 1991; Ciarletta, *et al.*, In: CURRENT

PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds., Greene Publishing Associates and Wiley-Interscience (Chapter 3Chapter 6, Chapter 7); Weinberger *et al.*, *Proc Natl Acad Sci USA* 77:6091-6095, 1980; Weinberger *et al.*, *Eur J Immun* 11:405-411, 1981; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

An ATLAS-X protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by vital (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by vital, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania species., malaria species. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions,

in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or energy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon re-exposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to energize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc Natl Acad Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and auto-antibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of auto-antibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can

be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic

vital diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-vital immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II a chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in

conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods: Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981; Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981; Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bowman *et al.*, *J Virology* 61:1992-1998; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *Cell Immunol* 133:327-341, 1991; Brown *et al.*, *J Immunol* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J Immunol* 144:3028-3033, 1990; and Mond and Brunswick In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, (eds.) Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *J Immunol* 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery *et al.*, *J Immunol* 134:536-544, 1995; Inaba *et al.*, *J Exp Med* 173:549-559, 1991; Macatonia *et al.*, *J Immunol* 154:5071-5079, 1995; Porgador *et al.*, *J Exp Med* 182:255-260, 1995; Nair *et al.*, *J Virol* 67:4062-4069, 1993; Huang *et al.*, *Science* 264:961-965, 1994; Macatonia *et al.*, *J Exp Med* 169:1255-1264, 1989; Bhardwaj *et al.*, *J Clin Investig* 94:797-807, 1994; and Inaba *et al.*, *J Exp Med* 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz *et al.*, *Cytometry* 13:795-808, 1992; Gorczyca *et al.*, *Leukemia* 7:659-670, 1993; Gorczyca *et al.*, *Cancer Res* 53:1945-1951, 1993; Itoh *et al.*, *Cell* 66:233-243, 1991; Zacharchuk, *J Immunol* 145:4037-4045, 1990; Zamai *et al.*, *Cytometry* 14:891-897, 1993; Gorczyca *et al.*, *Internat J Oncol* 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica *et al.*, *Blood* 84:111-117, 1994; Fine *et al.*, *Cell Immunol* 155: 111-122, 1994; Galy *et al.*, *Blood* 85:2770-2778, 1995; Toki *et al.*, *Proc Nat Acad Sci USA* 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

An ATLAS-X protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, *e.g.* in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as

thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (*i.e.,* in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson *et al. Cellular Biology* 15:141-151, 1995; Keller *et al., Mol. Cell. Biol.* 13:473-486, 1993; McClanahan *et al., Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y 1994; Hirayama *et al., Proc Natl Acad Sci USA* 89:5907-5911, 1992; McNiece and Briddeli, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben *et al., Exp Hematol* 22:353-359, 1994; Ploemacher, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Spooncer et *al.*, In: CULTURE OF HEMATOPOIETIC CELLS. Freshhey, *et al.*, (eds.) Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Sutherland, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.,* (eds.) Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

Tissue Growth Activity

An ATLAS-X protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of

tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendonitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a career as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, EPIDERMAL WOUND HEALING, pp. 71-112 (Maibach and Rovee, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Menz, *J. Invest. Dermatol* 71:382-84 (1978).

Activin/Inhibin Activity

An ATLAS-X protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin a family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-b group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale *et al.*, *Endocrinology* 91:562-572, 1972; Ling *et al.*, *Nature* 321:779-782, 1986; Vale *et al.*, *Nature* 321:776-779, 1986; Mason *et al.*, *Nature* 318:659-663, 1985; Forage *et al.*, *Proc Natl Acad Sci USA* 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (*e.g.*, act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Coligan *et al.*, eds. (Chapter 6.12, MEASUREMENT OF ALPHA AND BETA CHEMOKINES 6.12.1-6.12.28); Taub *et al. J Clin Invest* 95:1370-1376, 1995; Lind *et al. APMIS* 103:140-146, 1995; Muller *et al., Eur*

J Immunol 25: 1744-1748; Gruber*et al. J Immunol* 152:5860-5867, 1994; Johnston *et al., J Immunol* 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (*e.g.*, stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet *et al., J. Clin. Pharmacol.* 26:131-140, 1986; Burdick *et al., Thrombosis Res.* 45:413-419, 1987; Humphrey *et al., Fibrinolysis* 5:71-79 (1991); Schaub, *Prostaglandins* 35:467-474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell—cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan, *et al.*, Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai *et al.*, *Proc Natl Acad Sci USA* 84:6864-6868, 1987; Bierer *et al.*, *J. Exp. Med.* 168:1145-1156, 1988; Rosenstein *et al.*, *J. Exp. Med.* 169:149-160 1989; Stoltenborg *et al.*, *J Immunol Methods* 175:59-68, 1994; Stitt *et al.*, *Cell* 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell—cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor-Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

OTHER EMBODIMENTS

It is to be understood that while the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

What is claimed is:

1. An isolated nucleic acid molecule encoding a polypeptide comprising an amino acid sequence of a polypeptide at least 90% identical to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 SEQ ID NO:8, or the complement of said nucleic acid molecule.

2. The isolated nucleic acid molecule of claim 1, wherein said molecule hybridizes under stringent conditions to a nucleic acid sequence complementary to a nucleic acid molecule comprising a sequence selected from the group consisting of

nucleotides 1-2586 of SEQ ID NO:1,

nucleotides 1-5553of SEQ ID NO:3,

nucleotides 98-904 of SEQ ID NO:5, and

nucleotides 1-1074 of SEQ ID NO:7,

or the complement of said nucleic acid molecule.

3. The isolated nucleic acid molecule of claim 1, wherein said molecule encodes a polypeptide selected from the group consisting of

a polypeptide comprising the amino acid sequence of SEQ ID NO:2 or an amino acid sequence comprising one or more substitutions in the amino acid sequence of SEQ ID NO:2;

a polypeptide comprising the amino acid sequence of SEQ ID NO:4 or an amino acid sequence comprising one or more substitutions in the amino acid sequence of SEQ ID NO:4;

a polypeptide comprising the amino acid sequence of SEQ ID NO:6 or an amino acid sequence comprising one or more substitutions in the amino acid sequence of SEQ ID NO:6; and

a polypeptide comprising the amino acid sequence of SEQ ID NO:8 or an amino acid sequence comprising one or more substitutions in the amino acid sequence of SEQ ID NO:8;

or the complement of said nucleic acid molecule.

4. The nucleic acid molecule of claim 3, wherein one or more of said amino acid substitutions are conservative amino acid substitutions.

5. The nucleic acid molecule of claim 1, wherein said nucleotide sequence molecule encodes a polypeptide selected from the group consisting of

a polypeptide comprising the amino acid sequence of SEQ ID NO:2,

a polypeptide comprising the amino acid sequence of SEQ ID NO:4,

a polypeptide comprising the amino acid sequence of SEQ ID NO:6, and

a polypeptide comprising the amino acid sequence of SEQ ID NO:8,

or the complement of said nucleic acid molecule.

6. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of

nucleotides 1-2586 of SEQ ID NO:1,

nucleotides 1-5553of SEQ ID NO:3,

nucleotides 98-904 of SEQ ID NO:5, and

nucleotides 1-1074 of SEQ ID NO:7,

or the complement of said nucleic acid molecule.

7. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule comprises a nucleotide selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, and SEQ ID NO:7,

or the complement of said nucleic acid molecule.

8. A nucleic acid vector comprising the nucleic acid molecule of claim 1.

9. A host cell comprising the nucleic acid molecule of claim 1.

10. A pharmaceutical composition comprising the nucleic acid molecule of claim 1 and a pharmaceutically acceptable carrier.

11. An oligonucleotide less than 100 nucleotides in length and comprising at least 6 contiguous nucleotides of a nucleic acid molecule selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, and SEQ ID NO:7, or a complement thereof.

12. A substantially purified polypeptide comprising an amino acid sequence at least 80% identical to a polypeptide selected from the group consisting of

a polypeptide comprising the amino acid sequence of SEQ ID NO:2,

a polypeptide comprising the amino acid sequence of SEQ ID NO:4,

a polypeptide comprising the amino acid sequence of SEQ ID NO:6, and

a polypeptide comprising the amino acid sequence of SEQ ID NO:8.

13. The polypeptide of claim 12, wherein said polypeptide binds a phosphatase polypeptide or binds a cytokine..

14. The polypeptide of claim 12, wherein said polypeptide comprises the amino acid sequence of polypeptide selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, and SEQ ID NO:8.

15. A pharmaceutical composition comprising the polypeptide of claim 12 and a pharmaceutically acceptable carrier.

16. An antibody that selectively binds to the polypeptide of claim 12.

17. A pharmaceutical composition comprising the antibody of claim 16 and a pharmaceutically acceptable carrier.

18. A kit comprising in or more containers a compound selected from the group consisting of an ATLAS-X nucleic acid, an ATLAS-X polypeptide and an antibody to an ATLAS-X polypeptide, where X is 1, 2, 3, or 4.

19. The kit of claim 18, wherein said compound is present with a pharmaceutically acceptable carrier.

20. A method of producing a polypeptide, said method comprising culturing a cell comprising the nucleic acid molecule of claim 1 under conditions allowing for expression of a polypeptide encoded by said nucleic acid molecule.

21. A method of detecting the presence of a nucleic acid molecule of claim 1 in a sample, the method comprising contacting the sample with a nucleic acid probe or primer that selectively binds to the nucleic acid molecule and determining whether the nucleic acid probe or primer bound to the nucleic acid molecule of claim 1 is present in the sample.

22. A method of detecting the presence of the polypeptide of claim 12 in a sample, comprising contacting the sample with a compound that selectively binds to said polypeptide under conditions allowing for formation of a complex between said polypeptide and said compound, and detecting said complex, if present, thereby identifying said polypeptide in said sample.

23. A method of modulating the activity of the polypeptide of claim 12, the method comprising contacting a cell sample comprising said polypeptide with a compound that binds to said polypeptide in an amount sufficient to modulate the activity of the polypeptide.

24. The use of a therapeutic in the manufacture of a medicament for treating or preventing a syndrome associated with a human immune system disorder, wherein said therapeutic is selected from the group consisting of an ATLAS-X nucleic acid, an ATLAS-X polypeptide, and an antibody to an ATLAS-X polypeptide, wherein X is 1, 2, 3, or 4.

25. A method for screening for a modulator of activity or of latency or predisposition to an immune disorder, the method comprising:

contacting a test compound with the polypeptide of claim 12; and

determining if said test compound binds to said polypeptide,

wherein binding of said test compound to said polypeptide indicates the test compound a modulator of activity or of latency or predisposition to an immune disorder.

26. A method for screening for a modulator of activity or of latency or predisposition to an immune disorder, the method comprising:

administering a test compound to a test animal at increased risk for said disorder, wherein said test animal recombinantly expresses a polypeptide encoded by the nucleic acid sequence of claim 1;

measuring expression of the activity of said protein in said test animal;

measuring the activity of said protein in a control animal that recombinantly expresses said protein and is not at increased risk for any one of a from said disorder; and

comparing expression of said protein in said test animal and said control animal,

wherein a change in the activity of said protein in said test animal relative to said control animal indicates the test compound is a modulator of latency of any one of a from said disorder, and wherein said disorder is selected from the group consisting of an autoimmune disorder, an immune disorder, a T-lymphocyte-associated disorder, a cell-proliferation disorder, a cell differentiation disorder, and an immune deficiency order.

27. The method of claim 26, wherein said test animal is a recombinant test animal that expresses a test protein transgene or expresses said transgene under the control of a promoter at an increased level relative to a wild-type test animal, and wherein said promoter is not the native gene promoter of said transgene.

28. A method for determining the presence of or predisposition to a disease associated with altered levels of a polypeptide of claim 12 in a subject, the method comprising:

a) measuring the amount of the polypeptide in a sample from said subject; and

b) comparing the amount of said polypeptide in step (a) to the amount of the polypeptide present in a control sample,

wherein an alteration in the level of the polypeptide in step (a) as compared to the control sample indicates the presence of or predisposition to a disease in said subject.

29. The method of claim 28, wherein said subject is a human.

30. A method for determining the presence of or predisposition to a disease associated with altered levels of a nucleic acid molecule of claim 1 in a subject, the method comprising:

a) measuring the amount of the nucleic acid in a sample from the mammalian subject; and

b) comparing the amount of said nucleic acid in step (a) to the amount of the nucleic acid present in a control sample,

wherein an alteration in the level of the nucleic acid in step (a) as compared to the control sample indicates the presence or predisposition to said disease in said subject.

31. The method of claim 30, wherein said subject is a human.

32. A method of treating or preventing a pathological condition associated with an immune system disorder in a mammal, the method comprising administering to the subject the polypeptide of claim 12 to a subject in an amount sufficient to alleviate or prevent the pathological condition,

wherein the immune system associated disorder is selected from the group consisting of an autoimmune disorder, an immune disorder, a T-lymphocyte-associated disorder, a cell-proliferation disorder, a cell differentiation disorder, and an immune deficiency disorder.

33. The method of claim 32, wherein said subject is a human.

34. A method of treating or preventing a pathological condition associated with an immune disorder in a mammal, the method comprising administering to the subject the nucleic acid of claim 1 to a subject in an amount sufficient to treat or prevent the pathological condition,

wherein the immune system associated disorder is selected from the group consisting of an autoimmune disorder, an immune disorder, a T-lymphocyte-associated disorder, a cell-proliferation disorder, a cell differentiation disorder, and an immune deficiency disorder.

35. The method of claim 34, wherein said subject is a human.

36. A method of treating or preventing a pathological condition in a mammal, the method comprising administering to the subject the antibody of claim 16 in an amount sufficient to alleviate or prevent the pathological condition,

wherein the immune system associated disorder is selected from the group consisting of an autoimmune disorder, an immune disorder, a T-lymphocyte-associated disorder, a cell-proliferation disorder, a cell differentiation disorder, and an immune deficiency disorder.

37. The method of claim 36, wherein said subject is a human.

An ATLAS-1 Nucl ic Acid and Encoded Polypeptide According to the Invention

Translated Protein - Frame: 1 - Nucleotide 1 to 2586

```
  1 ATGATGAAGACGGAGCCACGGGGGCCCGGGGGTCCCCTCCGGAGC
    MetMetLysThrGluProArgGlyProGlyGlyProLeuArgSer

 46 GCCTCCCCGCACCGCAGCGCCTACGAGGCGGGCATCCAGGCGCTG
    AlaSerProHisArgSerAlaTyrGluAlaGlyIleGlnAlaLeu

 91 AAGCCGCCCGACGCGCCCGGCCCGACGAGGCACCCAAGGGGGCC
    LysProProAspAlaProGlyProAspGluAlaProLysGlyAla

136 CACCACAAGAAATATGGCTCCAACGTCCACCGCATCAAAAGTATG
    HisHisLysLysTyrGlySerAsnValHisArgIleLysSerMet

181 TTCCTGCAGATGGGCACGACGGCGGGGCCCTCGGGCGAGGCGGGC
    PheLeuGlnMetGlyThrThrAlaGlyProSerGlyGluAlaGly

226 GGCGGCGCGGGCCTGGCCGAGGCCCCACGGGCGTCCGAGCGCGGC
    GlyGlyAlaGlyLeuAlaGluAlaProArgAlaSerGluArgGly

271 GTGCGCCTGTCGCTGCCGCGGGCCAGCAGCCTGAACGAGAACGTG
    ValArgLeuSerLeuProArgAlaSerSerLeuAsnGluAsnVal

316 GACCACAGCGCCCTGCTGAAGCTGGGCACCAGCGTGTCGGAGCGC
    AspHisSerAlaLeuLeuLysLeuGlyThrSerValSerGluArg

361 GACCGGAAGCTGGACGTCGTGGTGCGCTTCAACGGCAGCACCGAG
    AspArgLysLeuAspValValValArgPheAsnGlySerThrGlu

406 GCGCTGGACAAGCTGGACGCTGACGCCGTGTCCCCCACGGTCAGC
    AlaLeuAspLysLeuAspAlaAspAlaValSerProThrValSer

451 CAGCTCAGCGCCGTCTTCGAGAAGGCCGACTCGAGGACCGGCCTC
    GlnLeuSerAlaValPheGluLysAlaAspSerArgThrGlyLeu

496 CACCGCGGGCCCGGGCTCCCCAGGGCCGCAGGGGTTCCCCAGGTC
    HisArgGlyProGlyLeuProArgAlaAlaGlyValProGlnVal

541 AACTCGAAGCTGGTCAGCAAGCGGTCCCGGGTGTTCCAGCCCCCG
    AsnSerLysLeuValSerLysArgSerArgValPheGlnProPro

586 CCGCCGCCGCCGCCCGCCCCGTCGGGGGATGCCCCGGCCGAGAAA
    ProProProProProAlaProSerGlyAspAlaProAlaGluLys

631 GAGCGATGCCCCGCAGGGCAGCAGCCCCCGCAGCACCGAGTGGCC
    GluArgCysProAlaGlyGlnGlnProProGlnHisArgValAla

676 CCTGCCCGGCCGCCCCCCAAGCCCCGGGAGGTGCGCAAGATTAAG
    ProAlaArgProProProLysProArgGluValArgLysIleLys
```

FIGURE 1A

721 CCGGTGGAGGTGGAGGAGAGCGGGGAGTCGGAGGCCGAGTCGGCG
ProValGluValGluGluSerGlyGluSerGluAlaGluSerAla

766 CCCGGGGAGGTGATCCAGGCCGAGGTTACGGTCCACGCGGCCCTG
ProGlyGluValIleGlnAlaGluValThrValHisAlaAlaLeu

811 GAGAATGGCAGCACCGTGGCAACTGCAGCCAGCCCCGCGCCCGAG
GluAsnGlySerThrValAlaThrAlaAlaSerProAlaProGlu

856 GAGCCAAAGGCCCAAGCGGCCCCGGAGAAGGAGGCGGCGGCGGTA
GluProLysAlaGlnAlaAlaProGluLysGluAlaAlaAlaVal

901 GCGCCGCCAGAGAGGGGGGTGGGCAATGGCCGGGCCCCGGACGTG
AlaProProGluArgGlyValGlyAsnGlyArgAlaProAspVal

946 GCCCCTGAGGAGGTAGATGAATCCAAGAAGGAGGACTTCTCGGAG
AlaProGluGluValAspGluSerLysLysGluAspPheSerGlu

991 GCGGACTTGGTGGACGTGAGCGCCTACAGTGGGCTCGGGGAGGAC
AlaAspLeuValAspValSerAlaTyrSerGlyLeuGlyGluAsp

1036 TCTGCGGGCAGTGCCCTGGAGGAGGACGACGAAGACGACGAGGAG
SerAlaGlySerAlaLeuGluGluAspAspGluAspAspGluGlu

1081 GATGGGGAGCCCCCCTACGAGCCCGAGTCGGGGTGCGTGGAGATC
AspGlyGluProProTyrGluProGluSerGlyCysValGluIle

1126 CCGGGGCTGTCGGAGGAGGAGGACCCAGCCCCGAGCCGGAAGATC
ProGlyLeuSerGluGluGluAspProAlaProSerArgLysIle

1171 CATTTCAGCACGGCGCCCATCCAAGGAGGGGCACTTTGTGTGGTC
HisPheSerThrAlaProIleGlnGlyGlyAlaLeuCysValVal

1216 CTTGATGGGGAGAGGCCTTCTGCAGGCATGGAGGAGGAGGAGGTG
LeuAspGlyGluArgProSerAlaGlyMetGluGluGluGluVal

1261 TTCAGCACTTACTCCAACGAGGATTACGATCGTCGCAACGAGGAT
PheSerThrTyrSerAsnGluAspTyrAspArgArgAsnGluAsp

1306 GTGGATCCCATGGCAGCCTCTGCTGAGTACGAGCTGGAGAAGCGT
ValAspProMetAlaAlaSerAlaGluTyrGluLeuGluLysArg

1351 GTGGAGAGGTTGGAGCTGTTCCCTGTGGAGCTGGAGAAGGACTCC
ValGluArgLeuGluLeuPheProValGluLeuGluLysAspSer

1396 GAGGGCCTGGGCATCAGCATCATCGGCATGGGCGCCGGGGCAGAC
GluGlyLeuGlyIleSerIleIleGlyMetGlyAlaGlyAlaAsp

1441 ATGGGCCTGGAGAAGCTGGGTATCTTCGTCAAGACCGTGACGGAG
MetGlyLeuGluLysLeuGlyIlePheValLysThrValThrGlu

1486 GGTGGTGCGGCCCATCGGGATGGCAGGATCCAGGTGAATGATCTC
GlyGlyAlaAlaHisArgAspGlyArgIleGlnValAsnAspLeu

1531 CTGGTGGAGGTGGATGGAACAAGTCTGGTGGGAGTGACCCAGAGC
LeuValGluValAspGlyThrSerLeuValGlyValThrGlnSer

FIGURE 1B

1576 TTCGCGGCGTCTGTGCTCCGGAACACCAAGGGCCGAGTGCGGTTT
PheAlaAlaSerValLeuArgAsnThrLysGlyArgValArgPhe

1621 ATGATTGGCCGGGAGCGGCCGGGAGAGCAGAGCGAAGTGGCCCAG
MetIleGlyArgGluArgProGlyGluGlnSerGluValAlaGln

1666 CTAATTCAGCAGACTTTGGAACAGGAGCGATGGCAGCGGGAGATG
LeuIleGlnGlnThrLeuGluGlnGluArgTrpGlnArgGluMet

1711 ATGGAGCAGAGATACGCCCAGTATGGGGAGGATGACGAGGAGACG
MetGluGlnArgTyrAlaGlnTyrGlyGluAspAspGluGluThr

1756 GGAGAGTATGCCACTGACGAGGATGAGGAGCTGAGCCCCACGTTC
GlyGluTyrAlaThrAspGluAspGluGluLeuSerProThrPhe

1801 CCGGGTGGTGAGATGGCCATCGAGGTGTTTGAGCTAGCGGAGAAC
ProGlyGlyGluMetAlaIleGluValPheGluLeuAlaGluAsn

1846 GAGGATGCACTGTCCCCTGTGGACATGGAGCCCGAGAAGCTGGTG
GluAspAlaLeuSerProValAspMetGluProGluLysLeuVal

1891 CACAAGTTCAAGGAGCTCCAGATCAAGCATGCGGTCACTGAGGCA
HisLysPheLysGluLeuGlnIleLysHisAlaValThrGluAla

1936 GAGATCCAGCAGCTGAAAAGAAAGCTGCAGAGCCTGGAGCAGGAG
GluIleGlnGlnLeuLysArgLysLeuGlnSerLeuGluGlnGlu

1981 AAGGGGCGCTGGCGGGTGGAGAAGGCGCAGTTGGAGCAGAGTGTG
LysGlyArgTrpArgValGluLysAlaGlnLeuGluGlnSerVal

2026 GAGGAGAACAAGGAGCGCATGGAGAAACTGGAAGGCTACTGGGGT
GluGluAsnLysGluArgMetGluLysLeuGluGlyTyrTrpGly

2071 GAGGCCCAGAGCCTGTGCCAGGCTGTGGACGAGCACCTGCGGGAG
GluAlaGlnSerLeuCysGlnAlaValAspGluHisLeuArgGlu

2116 ACTCAGGCGCAGTACCAGGCCCTGGAGCGCAAGTACAGCAAGGCC
ThrGlnAlaGlnTyrGlnAlaLeuGluArgLysTyrSerLysAla

2161 AAGCGCCTCATCAAGGACTACCAGCAGAAGGAGATCGAGTTCCTG
LysArgLeuIleLysAspTyrGlnGlnLysGluIleGluPheLeu

2206 AAAAAGGAGACTGCACAGCGTCGGGTTCTGGAGGAGTCGGAGCTG
LysLysGluThrAlaGlnArgArgValLeuGluGluSerGluLeu

2251 GCCAGAAAGGAGGAGATGGACAAGCTCCTGGACAAGGTGCCAAAT
AlaArgLysGluGluMetAspLysLeuLeuAspLysValProAsn

2296 AGCCATAACCTCGTCTTGGAACTGTTATGTGGCCTCTCTGGGGTC
SerHisAsnLeuValLeuGluLeuLeuCysGlyLeuSerGlyVal

2341 CAGGTTTCCTGGGCCTCTAAGAAGTTCAAAGGATGGGCTAAATAC
GlnValSerTrpAlaSerLysLysPheLysGlyTrpAlaLysTyr

2386 AGCAAGGTGAACCCCAAGTCCCTCCCCCAGAAGGCCTTTAAACTG
SerLysValAsnProLysSerLeuProGlnLysAlaPheLysLeu

FIGURE 1C

```
2431  TGGGGACACTCTCAAGAGGCACCCGGTGTGAGGCAGCACCATGGG
      TrpGlyHisSerGlnGluAlaProGlyValArgGlnHisHisGly

2476  CCTGAGGGGTTCCCGGGGCGCCAGACGCTGAAGATGACCGATGCC
      ProGluGlyPheProGlyArgGlnThrLeuLysMetThrAspAla

2521  GGAGGGGCCCTTTCCTATCGCCTGCCCGAAGGGCTTCTCCCTTCT
      GlyGlyAlaLeuSerTyrArgLeuProGluGlyLeuLeuProSer

2566  CTCCCACCCTCGGGCGTCACTTAGAGCGGCGGAAGCCCTTGTTCC
      LeuProProSerGlyValThr

2611  CAGTGCCAGTTCCCGTGGCCCCACTCTCGGTGTGATCTCTTTCTT
2656  CTCAGCAGCCCTGTGGACTCTCCGCCAGTTTGTGTGTCTGTCTCT
2701  GCTTCTTCCTACTCCTCACTTCCTTCCGCTCCCGCTCCCGCTCCC
2746  TCCCCAGGAATTGTGCGCCCTTTCTTCCTTTCTCCTTCTCCTGGG
2791  TCCCAAGAGGCTGTGAGCTCACCTGCCTCCCTTTCTCCCAGAGAA
2836  GGGTCAAAGGTCATTGGTGCTCCTTCTCCAGGATTGGAAGCCTTG
2881  GGGGGAAGGGTATCCAGAGGAACCGGTTCAATCCCACCCTTGTGC
2926  AGTTACCTGGCTGAATGGGGGTGTGTGTGTGTGTGTGTGTGTGTG
2971  TGTGTGAGAGAGTGTGCGGGGTGTGTGTGGGAGTGAGAGTGGGGG
3016  CGGGTTTGGTGTCTAATTTTTCTAGGCTCAGTTTTGGAAGGAGAG
3061  GGTTGGGTGGGAGGGGTCTGGTGACCCCCTGGACACAATGTAGGG
3106  AGGGTCCCCCTACACACCCCAGAAAGTTAGTTGTTGAAGGGAAGA
3151  AAAGAGAGCAGTTTGTGCTGAATCAGGATGGACCGAGAATGGCTT
3196  TGAGCAGGAAACCCCAATCCAGCCCAGAGGGTGCCTGGAAGAGGA
3241  GGACTCCAGCCAGCAGAGGATCTCGACCCTGGAATGGGCTCTTGA
3286  ATAAA
```

FIGURE 1D

An ATLAS-2 Nucleic Acid and Encoded Polyp ptide According to th Inv ntion

Translated Protein - Frame: 1 - Nucleotide 1 to 5553

```
  1 ATGGACCAGCCAGAGGCCCCCTGCTCCAGCACGGGGCCGCGCCTC
    MetAspGlnProGluAlaProCysSerSerThrGlyProArgLeu

 46 GCGGTGGCCCGCGAGCTGCTCCTGGCTGCGCTGGAGGAACTGAGC
    AlaValAlaArgGluLeuLeuLeuAlaAlaLeuGluGluLeuSer

 91 CAAGAGCAGCTGAAGCGCTTCCGCCACAAGCTGCGCGACGTGGGC
    GlnGluGlnLeuLysArgPheArgHisLysLeuArgAspValGly

136 CCGGACGGACGCAGCATCCCGTGGGGGCGGCTGGAGCGCGCGGAC
    ProAspGlyArgSerIleProTrpGlyArgLeuGluArgAlaAsp

181 GCCGTGGACCTCGCGGAGCAGCTGGCCCAGTTCTACGGCCCGGAG
    AlaValAspLeuAlaGluGlnLeuAlaGlnPheTyrGlyProGlu

226 CCTGCCCTGGAGGTGGCCCGCAAGACCCTCAAGAGGGCGGACGCG
    ProAlaLeuGluValAlaArgLysThrLeuLysArgAlaAspAla

271 CGCGACGTGGCGGCGCAGCTCCAGGAGCGGCGGCTGCAGCGGCTC
    ArgAspValAlaAlaGlnLeuGlnGluArgArgLeuGlnArgLeu

316 GGGCTCGGCTCCGGGACGCTGCTCTCCGTGTCCGAGTACAAGAAG
    GlyLeuGlySerGlyThrLeuLeuSerValSerGluTyrLysLys

361 AAGTACCGGGAGCACGTGCTGCAGCTGCACGCTCGGGTGAAGGAG
    LysTyrArgGluHisValLeuGlnLeuHisAlaArgValLysGlu

406 AGGAACGCCCGCTCCGTGAAGATCACCAAGCGCTTCACCAAGCTG
    ArgAsnAlaArgSerValLysIleThrLysArgPheThrLysLeu

451 CTCATCGCGCCCGAGAGCGCCGCCCCGGAGGAGGCGCTGGGGCCC
    LeuIleAlaProGluSerAlaAlaProGluGluAlaLeuGlyPro

496 GCGGAAGAGCCTGAGCCGGGGCGCGCGCGGCGCTCGGACACGCAC
    AlaGluGluProGluProGlyArgAlaArgArgSerAspThrHis

541 ACTTTCAACCGCCTCTTCCGCCGCGACGAGGAGGGCCGGCGGCCG
    ThrPheAsnArgLeuPheArgArgAspGluGluGlyArgArgPro

586 CTGACCGTGGTGCTGCAGGGCCCGGCGGGCATCGGCAAGACCATG
    LeuThrValValLeuGlnGlyProAlaGlyIleGlyLysThrMet

631 GCGGCCAAAAAGATCCTGTACGACTGGGCGGCGGGCAAGCTGTAC
    AlaAlaLysLysIleLeuTyrAspTrpAlaAlaGlyLysLeuTyr

676 CAGGGCCAGGTGGACTTCGCCTTCTTCATGCCCTGCGGCGAGCTG
    GlnGlyGlnValAspPheAlaPhePheMetProCysGlyGluLeu
```

FIGURE 2A

721 CTGGAGAGGCCGGGCACGCGCAGCCTGGCTGACCTGATCCTGGAC
LeuGluArgProGlyThrArgSerLeuAlaAspLeuIleLeuAsp

766 CAGTGCCCCGACCGCGGCGCGCCGGTGCCGCAGATGCTGGCCCAG
GlnCysProAspArgGlyAlaProValProGlnMetLeuAlaGln

811 CCGCAGCGGCTGCTCTTCATCCTGGACGGCGCGGACGAGCTGCCG
ProGlnArgLeuLeuPheIleLeuAspGlyAlaAspGluLeuPro

856 GCGCTGGGGGGCCCCGAGGCCGCGCCCTGCACAGACCCCTTCGAG
AlaLeuGlyGlyProGluAlaAlaProCysThrAspProPheGlu

901 GCGGCGAGCGGCGCGCGGGTGCTAGGCGGGCTGCTGAGCAAGGCG
AlaAlaSerGlyAlaArgValLeuGlyGlyLeuLeuSerLysAla

946 CTGCTGCCCACGGCCCTCCTGCTGGTGACCACGCGCGCCGCCGCC
LeuLeuProThrAlaLeuLeuLeuValThrThrArgAlaAlaAla

991 CCCGGGAGGCTGCAGGGCCGCCTGTGTTCCCCGCAGTGCGCCGAG
ProGlyArgLeuGlnGlyArgLeuCysSerProGlnCysAlaGlu

1036 GTGCGCGGCTTCTCCGACAAGGACAAGAAGAAGTATTTCTACAAG
ValArgGlyPheSerAspLysAspLysLysLysTyrPheTyrLys

1081 TTCTTCCGGGATGAGAGGAGGGCCGAGCGCGCCTACCGCTTCGTG
PhePheArgAspGluArgArgAlaGluArgAlaTyrArgPheVal

1126 AAGGAGAACGAGACGCTGTTCGCGCTGTGCTTCGTGCCCTTCGTG
LysGluAsnGluThrLeuPheAlaLeuCysPheValProPheVal

1171 TGCTGGATCGTGTGCACCGTGCTGCGCCAGCAGCTGGAGCTCGGT
CysTrpIleValCysThrValLeuArgGlnGlnLeuGluLeuGly

1216 CGGGACCTGTCGCGCACGTCCAAGACCACCACGTCAGTGTACCTG
ArgAspLeuSerArgThrSerLysThrThrThrSerValTyrLeu

1261 CTTTTCATCACCAGCGTTCTGAGCTCGGCTCCGGTAGCCGACGGG
LeuPheIleThrSerValLeuSerSerAlaProValAlaAspGly

1306 CCCCGGTTGCAGGGCGACCTGCGCAATCTGTGCCGCCTGGCCCGC
ProArgLeuGlnGlyAspLeuArgAsnLeuCysArgLeuAlaArg

1351 GAGGGCGTCCTCGGACGCAGGGCGCAGTTTGCCGAGAAGGAACTG
GluGlyValLeuGlyArgArgAlaGlnPheAlaGluLysGluLeu

1396 GAGCAACTGGAGCTTCGTGGCTCCAAAGTGCAGACGCTGTTTCTC
GluGlnLeuGluLeuArgGlySerLysValGlnThrLeuPheLeu

1441 AGCAAAAAGGAGCTGCCGGGCGTGCTGGAGACAGAGGTCACCTAC
SerLysLysGluLeuProGlyValLeuGluThrGluValThrTyr

1486 CAGTTCATCGACCAGAGCTTCCAGGAGTTCCTCGCGGCACTGTCC
GlnPheIleAspGlnSerPheGlnGluPheLeuAlaAlaLeuSer

1531 TACCTGCTGGAGGACGGCGGGGTGCCCAGGACCGCGGCTGGCGGC
TyrLeuLeuGluAspGlyGlyValProArgThrAlaAlaGlyGly

FIGURE 2B

1576 GTTGGGACACTCCTGCGTGGGGACGCCCAGCCGCACAGCCACTTG
VALGlyThrLeuLeuArgGlyAspAlaGlnProHisSerHisLeu

1621 GTGCTCACCACGCGCTTCCTCTTCGGACTGCTGAGCGCGGAGCGG
ValLeuThrThrArgPheLeuPheGlyLeuLeuSerAlaGluArg

1666 ATGCGCGACATCGAGCGCCACTTCGGCTGCATGGTTTCAGAGCGT
MetArgAspIleGluArgHisPheGlyCysMetValSerGluArg

1711 GTGAAGCAGGAGGCCCTGCGGTGGGTGCAGGGACAGGGACAGGGC
ValLysGlnGluAlaLeuArgTrpValGlnGlyGlnGlyGlnGly

1756 TGCCCCGGAGTGGCACCAGAGGTGACCGAGGGGGCCAAAGGGCTC
CysProGlyValAlaProGluValThrGluGlyAlaLysGlyLeu

1801 GAGGACACCGAAGAGCCAGAGGAGGAGGAGGAGGGAGAGGAGCCC
GluAspThrGluGluProGluGluGluGluGluGlyGluGluPro

1846 AACTACCCACTGGAGTTGCTGTACTGCCTGTACGAGACGCAGGAG
AsnTyrProLeuGluLeuLeuTyrCysLeuTyrGluThrGlnGlu

1891 GACGCGTTTGTGCGCCAAGCCCTGTGCCGGTTCCCGGAGCTGGCG
AspAlaPheValArgGlnAlaLeuCysArgPheProGluLeuAla

1936 CTGCAGCGAGTGCGCTTCTGCCGCATGGACGTGGCTGTTCTGAGC
LeuGlnArgValArgPheCysArgMetAspValAlaValLeuSer

1981 TACTGCGTGAGGTGCTGCCCTGCTGGACAGGCACTGCGGCTGATC
TyrCysValArgCysCysProAlaGlyGlnAlaLeuArgLeuIle

2026 AGCTGCAGATTGGTTGCTGCGCAGGAGAAGAAGAAGAAGAGCCTG
SerCysArgLeuValAlaAlaGlnGluLysLysLysLysSerLeu

2071 GGGAAGCGGCTCCAGGCCAGCCTGGGTGGCGGCAGCTGGCTGGGG
GlyLysArgLeuGlnAlaSerLeuGlyGlyGlySerTrpLeuGly

2116 ACCCAACTGGCTCCAGAAGTACCCTTTCGACCACCCTGCTGTGAC
ThrGlnLeuAlaProGluValProPheArgProProCysCysAsp

2161 ATCTGCCCCACACCTCCACCAGACCCTCGGCTCCTCCAGGGCAAG
IleCysProThrProProProAspProArgLeuLeuGlnGlyLys

2206 GCTTTTGCCAGAGTTCCTTTGAATATAGCTCCAATTCAGCCCCTG
AlaPheAlaArgValProLeuAsnIleAlaProIleGlnProLeu

2251 CCCAGGGGCTTGGCATCTGTTGAGAGGATGAATGTCACGGTGTTG
ProArgGlyLeuAlaSerValGluArgMetAsnValThrValLeu

2296 GCAGGGGCTGGGCCTGGGGACCCAAAGACCCATGCAATGACTGAC
AlaGlyAlaGlyProGlyAspProLysThrHisAlaMetThrAsp

2341 CCACTGTGCCATCTGAGCAGCCTCACGCTGTCCCACTGCAAACTC
ProLeuCysHisLeuSerSerLeuThrLeuSerHisCysLysLeu

2386 CCTGACGCGGTCTGCCGAGACCTTTCTGAGGCCCTGAGGGCAGCC
ProAspAlaValCysArgAspLeuSerGluAlaLeuArgAlaAla

FIGURE 2C

2431 CCCGCACTGACGGAGCTGGGCCTCCTCCACAACAGGCTCAGTGAG
ProAlaLeuThrGluLeuGlyLeuLeuHisAsnArgLeuSerGlu

2476 GCAGGACTGCGTATGCTGAGTGAGGGCCTAGCCTGGCCGCAGTGC
AlaGlyLeuArgMetLeuSerGluGlyLeuAlaTrpProGlnCys

2521 AGGGTGCAGACGGTCAGGGTACAGCTGCCTGACCCCCAGCGAGGG
ArgValGlnThrValArgValGlnLeuProAspProGlnArgGly

2566 CTCCAGTACCTGGTGGGTATGCTTCGGCAGAGCCCTGCCCTGACC
LeuGlnTyrLeuValGlyMetLeuArgGlnSerProAlaLeuThr

2611 ACCCTGGATCTCAGCGGCTGCCAACTGCCCGCCCCCATGGTGACC
ThrLeuAspLeuSerGlyCysGlnLeuProAlaProMetValThr

2656 TACCTGTGTGCAGTCCTGCAGCACCAGGGATGCGGCCTGCAGACC
TyrLeuCysAlaValLeuGlnHisGlnGlyCysGlyLeuGlnThr

2701 CTCAGCCTCTCGCTTCCTTCTGACCCGACCCCGAGTTCTTTCTCC
LeuSerLeuSerLeuProSerAspProThrProSerSerPheSer

2746 GGACGGTGTCGAGAACCCGGGCGCCGGCTGGGGCTGGAGTCTCGC
GlyArgCysArgGluProGlyArgArgLeuGlyLeuGluSerArg

2791 TGGCCTCGGAGCGCCCCCGAGCCCTCGGGCGACAGCGAGGCGAGG
TrpProArgSerAlaProGluProSerGlyAspSerGluAlaArg

2836 ACCCAGGTGGAGGCGGCCGGGGGCGCGGGCGGAGGGAGGAGGCGC
ThrGlnValGluAlaAlaGlyGlyAlaGlyGlyGlyArgArgArg

2881 GGGAGGGAACCCCCGGCCCGCGGGCCCCACCCACAGCCGCCCCGG
GlyArgGluProProAlaArgGlyProHisProGlnProProArg

2926 GACGCAGCTCGGGGTCCAGGCTCGAGCTTTGCTCACTCAGGGCGC
AspAlaAlaArgGlyProGlySerSerPheAlaHisSerGlyArg

2971 TTCGTGCAGGGAACGCCAGGCCCCCGGACGCGACCCACGCGGCCG
PheValGlnGlyThrProGlyProArgThrArgProThrArgPro

3016 CTGCCAGCGGGGACCGAGGGGAGCCGGGGCCGCGGCCGCGAGTCC
LeuProAlaGlyThrGluGlySerArgGlyArgGlyArgGluSer

3061 ACGTCCCGCCCCCGGGCCCGGCCCAGCGACCGCCCCCGCCGCCCA
ThrSerArgProArgAlaArgProSerAspArgProArgArgPro

3106 GGGACCGCCCCCGCCTCCCAGCGACCGCCCGGGCCCTCGGGGCGG
GlyThrAlaProAlaSerGlnArgProProGlyProSerGlyArg

3151 GGACCGCGGACCTTCCTGGTGGCGCGGCAGCCGGGCGGCTCCTCC
GlyProArgThrPheLeuValAlaArgGlnProGlyGlySerSer

3196 TTCCTCCCGGCCCTGGCGTGGAGCAGAGGGACACAGGTTCCCACG
PheLeuProAlaLeuAlaTrpSerArgGlyThrGlnValProThr

3241 CTGGCGCCCGGCGACCGGGTGGGGCTGCGGCCGCTCAGGCCCAGC
LeuAlaProGlyAspArgValGlyLeuArgProLeuArgProSer

FIGURE 2D

```
3286  AGCTCCATGGAGGACGCCGGCGAGGACCCCACCACGTTTGCTGCC
      SerSerMetGluAspAlaGlyGluAspProThrThrPheAlaAla

3331  CACTCTCTGCCCAGTGACCCCCGTCTCTTGGCCACTGTGACCAAC
      HisSerLeuProSerAspProArgLeuLeuAlaThrValThrAsn

3376  GCATACCTGGGCACACGAGTGTTTCACGACACGCTGCACGTGAGC
      AlaTyrLeuGlyThrArgValPheHisAspThrLeuHisValSer

3421  GGCGTGTACAATGGGGCTGGCGGGGACACGCACCGGGCCATGCTG
      GlyValTyrAsnGlyAlaGlyGlyAspThrHisArgAlaMetLeu

3466  CCCAGCCCCCTCAACGTCCGGCTGGAGGCCCCTGCAGGGATGGGG
      ProSerProLeuAsnValArgLeuGluAlaProAlaGlyMetGly

3511  GAGCAGCTGACCGAGACCTTCGCCCTGGACACCAACACAGGCTCC
      GluGlnLeuThrGluThrPheAlaLeuAspThrAsnThrGlySer

3556  TTTCTTCACACCCTGGAGGGCCCCCGCTTCCGGGCCTCCCAGTGC
      PheLeuHisThrLeuGluGlyProArgPheArgAlaSerGlnCys

3601  ATCTATGCGCATCGCACGCTGCCCCACGTGCTGGCTTTCCGAGTG
      IleTyrAlaHisArgThrLeuProHisValLeuAlaPheArgVal

3646  TCCATCGCCCGCCTGGCCCCGGGGAGCGGGCCCATCACGCTGCTC
      SerIleAlaArgLeuAlaProGlySerGlyProIleThrLeuLeu

3691  CTGCGGTCAGCCTTCTCCCCAGAAAGCCCAGACCTGGACCTGCAT
      LeuArgSerAlaPheSerProGluSerProAspLeuAspLeuHis

3736  CAGGGTCCTGACTTCCAGGGAGCCCGGTACCTGTATGGCCACACC
      GlnGlyProAspPheGlnGlyAlaArgTyrLeuTyrGlyHisThr

3781  CTCACCCCTGAGCAGCCCGGGGGGCCACAGCAAGAGGTACACATG
      LeuThrProGluGlnProGlyGlyProGlnGlnGluValHisMet

3826  CTGTGGACACCAGCACCCCCAGACCTGACCCTTGGGGAAGGTGAG
      LeuTrpThrProAlaProProAspLeuThrLeuGlyGluGlyGlu

3871  GAGGCTAGGACGTGGGACTTCCTGACAGCAGTGGGCGGCAGCCAG
      GluAlaArgThrTrpAspPheLeuThrAlaValGlyGlySerGln

3916  GCTGAGGCTCAGGCCTGCCTCACTGAGGCCCTGCAGCTGCAGGCC
      AlaGluAlaGlnAlaCysLeuThrGluAlaLeuGlnLeuGlnAla

3961  AGGGGAGCTCTGTATACGGCTCACGCACAGGCCTGGGCCCAGCTC
      ArgGlyAlaLeuTyrThrAlaHisAlaGlnAlaTrpAlaGlnLeu

4006  TGGGTAGAATGTGGCTTGGACGTGGTGGGCCCCCTGCAGCTGCGC
      TrpValGluCysGlyLeuAspValValGlyProLeuGlnLeuArg

4051  CAGGCCCTGCGTGGCTCCCTCTACTACCTGCTCAGTGCCCTGCCC
      GlnAlaLeuArgGlySerLeuTyrTyrLeuLeuSerAlaLeuPro

4096  CAGCCCAAGGCCCCAGGATACATCTGCCATGGCCTCAGTCCTGGG
      GlnProLysAlaProGlyTyrIleCysHisGlyLeuSerProGly
```

FIGURE 2E

4141 GGCCTCTCCAATGGGAGCCGTGAGGAATGCTACTGGGGCCACGTC
GlyLeuSerAsnGlySerArgGluGluCysTyrTrpGlyHisVal

4186 TTCTGGGACCAGGACCTCTGGATGTTCCCGAGTATCCTGATGTTC
PheTrpAspGlnAspLeuTrpMetPheProSerIleLeuMetPhe

4231 CACCCAGAAGCCGCCAGGGCCATCCTGGAGTACCGCATCCGCACG
HisProGluAlaAlaArgAlaIleLeuGluTyrArgIleArgThr

4276 CTGGACGGGGCCCTGGAGAACGCCCAGAACCTGGGCTACCAGGGA
LeuAspGlyAlaLeuGluAsnAlaGlnAsnLeuGlyTyrGlnGly

4321 GCCAAGTTTGCCTGGGAGAGTGCAGACTCCGGCCTAGAGGTTTGC
AlaLysPheAlaTrpGluSerAlaAspSerGlyLeuGluValCys

4366 CCTGAGGACATTTACGGAGTCCAGGAGGTCCACGTCAACGGGGCC
ProGluAspIleTyrGlyValGlnGluValHisValAsnGlyAla

4411 GTGGTGTTGGCCTTCGAGCTGTACTACCATACCACCCAGGACCTG
ValValLeuAlaPheGluLeuTyrTyrHisThrThrGlnAspLeu

4456 CAGCTATTTCGAGAGGCTGGTGGCTGGGACGTGGTCAGGGCTGTG
GlnLeuPheArgGluAlaGlyGlyTrpAspValValArgAlaVal

4501 GCCGAGTTTTGGTGCAGTCGTGTTGAGTGGAGCCCCAGGGAGGAA
AlaGluPheTrpCysSerArgValGluTrpSerProArgGluGlu

4546 AAGTACCACCTGAGGGGAGTCATGTCCCCCGACGAGTACCATTCA
LysTyrHisLeuArgGlyValMetSerProAspGluTyrHisSer

4591 GGGGTCAACAACTCTGTGTACACCAACGTCCTGGTCCAGAACAGC
GlyValAsnAsnSerValTyrThrAsnValLeuValGlnAsnSer

4636 CTGCGCTTTGCTGCTGCCCTGGCCCAGGACCTGGGTCTTCCCATC
LeuArgPheAlaAlaAlaLeuAlaGlnAspLeuGlyLeuProIle

4681 CCCAGCCAGTGGCTGGCGGTGGCTGACAAGATCAAGGTACCCTTT
ProSerGlnTrpLeuAlaValAlaAspLysIleLysValProPhe

4726 GACGTGGAGCAGAACTTCCACCCGGAGTTCGATGGGTATGAGCCT
AspValGluGlnAsnPheHisProGluPheAspGlyTyrGluPro

4771 GACCCTCGAGTCTGTCCTGGAACACCTTCCAGTCAGCGGCACCTC
AspProArgValCysProGlyThrProSerSerGlnArgHisLeu

4816 CCTGTAGGAGAGGTGGTGAAGCAGGCAGACGTCGTGCTCCTGGGA
ProValGlyGluValValLysGlnAlaAspValValLeuLeuGly

4861 TACCCAGTCCCCTTCTCCCTGAGTCCTGATGTTCGCAGGAAAAAT
TyrProValProPheSerLeuSerProAspValArgArgLysAsn

4906 CTGGAGATTTACGAGGCTGTGACGTCCCCCCAGGGCCCCGCCATG
LeuGluIleTyrGluAlaValThrSerProGlnGlyProAlaMet

4951 ACCTGGAGCATGTTTGCTGTGGGCTGGATGGAGCTGAAGGACGCA
ThrTrpSerMetPheAlaValGlyTrpMetGluLeuLysAspAla

FIGURE 2F

4996 GTGCGGGCCCGGGGCCTCCTGGACAGGAGCTTTGCCAACATGGCT
ValArgAlaArgGlyLeuL uAspArgSerPheAlaAsnMetAla

5041 GAACCCTTCAAGGTGTGGACGGAGAATGCAGACGGGTCAGGCGCT
GluProPheLysValTrpThrGluAsnAlaAspGlySerGlyAla

5086 GTGAACTTCCTGACAGGCATGGGGGGCTTCCTGCAGGCGGTGGTC
ValAsnPheLeuThrGlyMetGlyGlyPheLeuGlnAlaValVal

5131 TTCGGGTGCACGGGGTTCAGGGTCACCCGAGCGGGTGTGACCTTT
PheGlyCysThrGlyPheArgValThrArgAlaGlyValThrPhe

5176 GACCCTGTGTGTCTGTCGGGGATCTCCAGAGTGAGCGTCTCCGGC
AspProValCysLeuSerGlyIleSerArgValSerValSerGly

5221 ATCTTCTACCAGGGGAACAAGCTCAACTTCTCTTTTTCCGAGGAC
IlePheTyrGlnGlyAsnLysLeuAsnPheSerPheSerGluAsp

5266 TCCGTGACCGTGGAGGTCACAGCTCGAGCAGGGCCCTGGGCTCCT
SerValThrValGluValThrAlaArgAlaGlyProTrpAlaPro

5311 CACCTGGAGGCTGAGCTGTGGCCATCCCAGTCCCGGCTCTCCCTG
HisLeuGluAlaGluLeuTrpProSerGlnSerArgLeuSerLeu

5356 TTGCCAGGACACAAGGTCTCCTTTCCCCGCTCGGCTGGCCGGATA
LeuProGlyHisLysValSerPheProArgSerAlaGlyArgIle

5401 CAAATGTCACCCCCGAAGCTGCCTGGAAGTTCCAGCTCCGAGTTC
GlnMetSerProProLysLeuProGlySerSerSerSerGluPhe

5446 CCTGGGAGGACTTTTTCAGATGTTAGGGACCCGCTCCAGAGCCCC
ProGlyArgThrPheSerAspValArgAspProLeuGlnSerPro

5491 CTCTGGGTCACCCTGGGTTCCTCCAGCCCCACCGAGTCACTCACT
LeuTrpValThrLeuGlySerSerSerProThrGluSerLeuThr

5536 GTGGACCCTGCCTCTGAATAATCAGGAACGGTGGCTTCAGAGACG
ValAspProAlaSerGlu

5581 TCTCTTGGGCCTTCCCTCTGGCCACGTCTGCACCCACCCCTCCTG
5626 GGCACCCTCCTAGCCTGCCATCCCTCACCTGCAGCCAGGCTCTCA
5671 GGGAAGGTCCATGCTGCTTGGCCTGAGTTCAAGGCTTTCTGCCTG
5716 TAGCCTGGACTCCCGTGGACCCCCGTGGGCAGGTGGCTTCCCCGT
5761 GGCATCTCCACACCGCCTCTGCCTGCCCCTGTGGACTGATGCTAT
5806 CGCGCACCGTCCCACGACCCCACCCCGAGCTCCTGAAGCCGGGGT
5851 CTGAGCCTGCATCACCTCTGGCCTCTCATCCCCCACTCTCCTGAG
5896 AGCAGTGGTCACAGCGGCCGGCCGCTCTGCTGAGAAGGCAGAGAG
5941 GCAGGCTCAGGCCTCAGCGTGGACAGCAGGGATAAGGGGCACGAA
5986 GGACGGGGACTCGGCCCCTTCAGAATTCCTCAGGACTCTCAGGTG
6031 CAGCTTTGCCAAAAAGGAACTTTTCATGTCATGCAGTTGAGGGGA
6076 CTTAGTCTCAATCCCAGGCTCCTCTTGACTCTGGGCAGCTTTAAT
6121 CAGGTTGGGCAGCCTCTGCTACAGCGTGGGGTGGGATGGCTCTCT
6166 TCCCTCAGCCACGCCGCTTGTGAGGACAGAGGTGGGGGAGTGGGA
6211 AGTGGGAAGTCACCAGAGAACAGGAGAGGGATTTGAGGGCGAGAC
6256 CCCAGCGCTCTCCACGGACCAGCCAGAGGGACTGGAGCCAGGTGT
6301 GCATGGGTTCAAGGCCCTGGCCCTGCCCAGCCTTTGTCTTGGGAG
6346 CTCAGCCCCAGGGTTCGGTCGTCAGCAGTTTCCCAAGAACAAGAT

FIGURE 2G

6391 GTGATGGCATCTGCTGCTGAAACCCTGATGAGGACCAGGCCCCCT
6436 GCACCGCTGTCAGCCTGAGGAATTAA

FIGURE 2H

An ATLAS-3 Nucleic Acid and Encoded Polypeptide According to th Inv ntion

Translated Protein - Frame: 2 - Nucleotide 98 to 904

```
  1 GCTGATTGTCCATCAAAGATGACAAATTTGGTTTTGAGTATTGTT
 46 ATGAACTCATGAACAGAAACACATTTGATGGAGTCCCTTTGTACC

 91 AATTAGGATGCTGCAGACACTGAACGAGGAGCCAGTGACACCAGA
           MetLeuGlnThrLeuAsnGluGluProValThrProGl

136 GCCGGAAGTGGAACCGCCCATTGCCCCCGAGCTCAAGCAAGGGCT
    uProGluValGluProProIleAlaProGluLeuLysGlnGlyLe

181 GTATGAGCTCTCAGCAAGCAACTTTGAGCTGCACGTTGCACAAGG
    uTyrGluLeuSerAlaSerAsnPheGluLeuHisValAlaGlnGl

226 CGACCACTTTATCAAGTTCTTCGCTCCGTGGTGTGGTCACTGCAA
    yAspHisPheIleLysPhePheAlaProTrpCysGlyHisCysLy

271 AGCCCTGGCTCCAACCTGGGAGCAGCTGGCTCTGGGCCTTGAACA
    sAlaLeuAlaProThrTrpGluGlnLeuAlaLeuGlyLeuGluHi

316 TTCCGAAACTGTCAAGATTGGCAAGGTTGATTGTACACAGCACTA
    sSerGluThrValLysIleGlyLysValAspCysThrGlnHisTy

361 TGAACTCTGCTCCGGAAACCAGGTTCGTGGCTATCCCACTCTTCT
    rGluLeuCysSerGlyAsnGlnValArgGlyTyrProThrLeuLe

406 CTGGTTCCGAGATGGGAAAAAGGTGGATCAGTACAAGGGAAAGCG
    uTrpPheArgAspGlyLysLysValAspGlnTyrLysGlyLysAr

451 GGATTTGGAGTCACTGAGGGAGTACGTGGAGTCGCAGCTGCAGCG
    gAspLeuGluSerLeuArgGluTyrValGluSerGlnLeuGlnAr

496 CACAGAGACTGGAGCGACGGAGACCGTCACGCCCTCAGAGGCCCC
    gThrGluThrGlyAlaThrGluThrValThrProSerGluAlaPr

541 GGTGCTGGCAGCTGAGCCCGAGGCTGACAAGGGCACTGTGTTGGC
    oValLeuAlaAlaGluProGluAlaAspLysGlyThrValLeuAl

586 ACTCACTGAAAATAACTTCGATGACACCATTGCAGAAGGAATAAC
    aLeuThrGluAsnAsnPheAspAspThrIleAlaGluGlyIleTh

631 CTTCATCAAGTTTTATGCTCCATGGTGTGGTCATTGTAAGACTCT
    rPheIleLysPheTyrAlaProTrpCysGlyHisCysLysThrLe

676 GGCTCCTACTTGGGAGGAACTCTCTAAAAAGGAATTCCCTGGTCT
    uAlaProThrTrpGluGluLeuSerLysLysGluPheProGlyLe

721 GGCGGGGGTCAAGATCGCCGAAGTAGACTGCACTGCTGAACGGAA
    uAlaGlyValLysIleAlaGluValAspCysThrAlaGluArgAs
```

FIGURE 3A

```
766   TATCTGCAGCAAGTATTCGGTACGAGGCTACCCCACGTTATTGCT
      nIleCysSerLysTyrSerValArgGlyTyrProThrLeuLeuLe

811   TTTCCGAGGAGGGAAGAAAGTCAGTGAGCACAGTGGAGGCAGAGA
      uPheArgGlyGlyLysLysValSerGluHisSerGlyGlyArgAs

856   CCTTGACTCGTTACACCGCTTTGTCCTGAGCCAAGCGAAAGACGA
      pLeuAspSerLeuHisArgPheValLeuSerGlnAlaLysAspGl

901   ACTTTAGGAACACAGTTGGAGGTCACCTCTCCTGCCCAGCTCCCG
      uLeu

946   CACCCTGCGTTTAGGAGTTCAGTCCCACAGAGGCCACTGGGTTCC
991   CAGTGGTGGCTGTTCAGAAAGCAGAACATACTAAGCGTGAGGTAT
1036  CTTCTTTGTGTGTGTGTTTTCCAAGCCAACACACTCTACAGATTC
1081  TTTATTAAGTTAAGTTTCTCTAAGTAAATGTGTAACTCATGGTCA
1126  CTGTGTAAACATTTTCAGTGGCGATATATCCCCTTTGACCTTCTC
1171  TTGATGAAATTTACATGGTTTCCTTTGAGACTAAAATAGCGTTGA
1216  GGGAAATGAAATTGCTGGACTATTTGTGGCTCCTGAGTTGAGTGA
1261  TTTTGGTGAAAGAAAGCACATCCAAAGCATAGTTTACCTGCCCAC
1306  GAGTTCTGGAAAGGTGGCCTTGTGGCAGTATTGACGTTCCTCTGA
1351  TCTTAAGGTCACAGTTGACTCAATACTGTGTTGGTCCGTAGCATG
1396  GAGCAGATTGAAATGCAAAAACCCACACCTCTGGAAGATACCTTC
1441  ACGGCCGCTGCTGGAGCTTCTGTTGCTGTGAATACTTCTCTCAGT
1486  GTGAGAGGTTAGCCGTGATGAAAGCAGCGTTACTTCTGACCGTGC
1531  CTGAGTAAGAGAATGCTGATGCCATAACTTTATGTGTCGATACTT
1576  GTCAAATCAGTTACTGTTCAGGGGATCCTTCTGTTTCTCACGGGG
1621  TGAAACATGTCTTTAGTTCCTCATGTTAACACGAAGCCAGAGCCC
1666  ACATGAACTGTTGGATGTCTTCCTTAGAAAGGGTAGGCATGGAAA
1711  ATTCCACGAGGCTCATTCTCAGTATCTCATTAACTCATTGAAAGA
1756  TTCCAGTTGTATTTGTCACCTGGGGTGACAAGACCAGACAGGCTT
1801  TCCCAGGCCTGGGTATCCAGGGAGGCTCTGCAGCCCTGCTGAAGG
1846  GCCCTAACTAGAGTTCTAGAGTTTCTGATTCTGTTTCTCAGTAGT
1891  CCTTTTAGAGGCTTGCTATACTTGGTCTGCTTCAAGGAGGTCGAC
1936  CTTCTAATGTATGAAGAATGGATGCATTTGATCTCAAGACCAAA
1981  GACAGATGTCAGTGGGCTGCTCTGGCCCTGGTGTGCACGGCTGTG
2026  GCAGCTGTTGATGCCAGTGTCCTCTAACTCATGCTGTCCTTGTGA
2071  TTAAACACCTCTATCTCCCTTGGGAATAAGCACATACAGGCTTAA
2116  GCTCTAAGATAGATAGGTGTTTGTCCTTTTACCATCGAGCTACTT
2161  CCCATAATAACCACTTTGCATCCAACACTCTTCACCCACCTCCCA
2206  TACGCAAGGGGATGTGGATACTTGGCCCAAAGTAACTGGTGGTAG
2251  GAATCTTAGAAACAAGACCACTTATACTGTCTGTCTGAGGCAGAA
2296  GATAACAGCAGCATCTCGACCAGCCTCTGCCTTAAAGGAAATCTT
2341  TATTAATCACGTATGGTTCACAGATAATTCTTTTTTTAAAAAAAC
2386  CCAACCTCCTAGAGAAGCACAACTGTCAAGAGTCTTGTACACACA
2431  ACTTCAGCTTTGCATCACGAGTCTTGTATTCCAAGAAAATCAAAG
2476  TGGTACAATTTGTTTGTTTACACTATGATACTTTCTAAATAAACT
2521  CTTTTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
```

FIGURE 3B

An ATLAS-4 Nucleic Acid and Encoded Polyp ptide According to the Invention

Translated Protein - Frame: 1 - Nucleotide 1 to 1074

1 ATGCCTAAGCCTTCCCCTGCCTCCGTGGGTTCCTGTGCAGCCCGA
MetProLysProSerProAlaSerValGlySerCysAlaAlaArg

46 GCCTCCCCAACGAATACCATCCCCTGCTCCACGGCGCCCAGTCCC
AlaSerProThrAsnThrIleProCysSerThrAlaProSerPro

91 ATCGACCACCCAAGGGCTGACGAGTACGAGCTCATGGCATGGGAC
IleAspHisProArgAlaAspGluTyrGluLeuMetAlaTrpAsp

136 TGGCAGGCAGCTCCACCTGCAGCCCCAGTGCGGGATCCACTCGGT
TrpGlnAlaAlaProProAlaAlaProValArgAspProLeuGly

181 GAAGCCAGCTGGGCTCCTGGTCTGGTGGGGACGTGGAGAGTCTTT
GluAlaSerTrpAlaProGlyLeuValGlyThrTrpArgValPhe

226 ATATCTAGCTCAGAGATTGTAAACACACCAATCAGCACCCTGTGT
IleSerSerSerGluIleValAsnThrProIleSerThrLeuCys

271 CTAGCTCAAGGAGGACAGGCAAGGGTGCAGGTTTTCGAGAATGCG
LeuAlaGlnGlyGlyGlnAlaArgValGlnValPheGluAsnAla

316 TCAGTAAGGACCACTAAATCCGACCTTCCTCGGTCCTCCATGTGG
SerValArgThrThrLysSerAspLeuProArgSerSerMetTrp

361 TCTGGGAGGAAAACTAGTGTTTCTGCTGCTGCGTCGAAGGAAATA
SerGlyArgLysThrSerValSerAlaAlaAlaSerLysGluIle

406 AGCAAAGAAATCTCCAAAGGTCCACAAAAACCCCCGGGCTATCGG
SerLysGluIleSerLysGlyProGlnLysProProGlyTyrArg

451 TTATGTCCCCTTCAAGCTGTAGGGGGAGGGGAATTTGGCCCAACC
LeuCysProLeuGlnAlaValGlyGlyGlyGluPheGlyProThr

496 CGGGTGCATGTCCCCTTCTCCCTCTCTGATTTAAAGCAGATCAAG
ArgValHisValProPheSerLeuSerAspLeuLysGlnIleLys

541 GCAGACCTGGGGAAGTTTTCAGATGATCCTGATAGAATCGAGGCC
AlaAspLeuGlyLysPheSerAspAspProAspArgIleGluAla

586 ATCAAGCTACAGATGGTCTTACAAATGGAACCCCAAAAGAGTTCA
IleLysLeuGlnMetValLeuGlnMetGluProGlnLysSerSer

631 ACTAACAACTTCTACCGAGGACCCCTGGATCAACCCACTGGCACT
ThrAsnAsnPheTyrArgGlyProLeuAspGlnProThrGlyThr

676 TCCCCTGGCCTAGAGAGTTCCCCTCTGAAGGACACCGCAACTGCA
SerProGlyLeuGluSerSerProLeuLysAspThrAlaThrAla

FIGURE 4A

```
721  GGGCCCCTTCTTTGCCCCATCCAGCAGGAAGTAGCTAGAGTGGTC
     GlyProLeuLeuCysProIleGlnGlnGluValAlaArgValVal

766  ATCGGCCAAATTGCCAACAGCAGTTGGGGTGTCCTGTTTAGAGGG
     IleGlyGlnIleAlaAsnSerSerTrpGlyValLeuPheArgGly

811  GGGATTGAGAGGACTCGGGACCTGCAGCCCGCCATGCCTAAGCCT
     GlyIleGluArgThrArgAspLeuGlnProAlaMetProLysPro

856  TCCCCAACCTCTGTGGGTTCCTGTGCAGCCCGAGCCTCCCCGACG
     SerProThrSerValGlySerCysAlaAlaArgAlaSerProThr

901  AATACCATCCCCTGCTCCATGGCACCCAGTCCCGTCGACTACCCA
     AsnThrIleProCysSerMetAlaProSerProValAspTyrPro

946  AGGGCTGAGGAGTACAAGTTCATGGCGCGGGACTGGCAGACAGCT
     ArgAlaGluGluTyrLysPheMetAlaArgAspTrpGlnThrAla

991  CCACCTGCAGCCCCAGTGCGGGATCCACTGGGTGAAGCCAGCTGG
     ProProAlaAlaProValArgAspProLeuGlyGluAlaSerTrp

1036 GCTCCTGAGTCTGGTGGGGACGTGGAGAGTCTTTATATCTAGCTC
     AlaProGluSerGlyGlyAspValGluSerLeuTyrIle

1081 AGGGATTGTAAACACACCAATCAGCACCCTGTGTCTAGCTCAAGG
1126 TTTGTGAGTGCACCAATCAACACTCTGTATCTAGCTGCTCTGGTG
1171 GGGCCTTGGAGAACTTTTATGTCTAGCTCAGGGATTGTAAATACC
1216 CCAACCAGCACCCTGTGTTTAGCTCAAGGTTTGTGAGTGCACCAA
1261 TCGACACTCTGTATCTAGCTGCTCTGATGAGGACGTGGAGGACCT
1306 TTATGTCTAGCTCAAGGATTGTTAATACATCAATCGGCACTCTGT
1351 ATCTAGCTCAAGGTTTGTAAATACACCAATCAGCACCCTCTGTTT
1396 AGCTCAAGGTTTGTGAGTGCACCAATCGACACTGTGTATCTAGCT
1441 GCTCTGGTGGGGCCTTGGTGAACCTTTATGTCTAGCTCAGGGATT
1486 GTAAATACCCCAATCAGCACCCTGTGTTTAGCTCAAGGTTTGTGA
1531 GTGCACCAATCGACACTCTGTATCTAGCTGCTCTGGTGGGGCCCT
1576 GGAGAACCTGTGTGTAGAAACTCTGTATCTAACTAATCTGATGGG
1621 GACGTGGAGAACCTTTGTATCTAGCTCAGGGATTGTAAACGCACC
1666 AATCAGCGCCCTGACAAAACAGGCCACTCGGCTCTACCAATCAGC
1711 AGGATGTGGGTGGGGCCAGAAAAGACAATAAAAGCAGGCTGCCCG
1756 AGCCAGCATTGGCAACCTTCTCGGGTCCCCTTCCACACTGTGGAA
1801 GCTTTGTTCTTTCGCTCTTTGCAATAAA
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FIGURE 4B